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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:46:58 ; Search time 226 Seconds
(without alignments)
7833.856 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 1 catagtgccacaagcttacc.....atgagcttaataagaagcc 996

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patente NA.*
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	16.0	990	US-09-710-279-413	Sequence 413, App
2	159	16.0	996	US-09-134-001C-2421	Sequence 2421, Ap
3	159	16.0	2975	US-09-710-279-3345	Sequence 3345, Ap
4	159	16.0	4114	US-09-710-279-4184	Sequence 4184, Ap
5	146	14.7	11466	US-08-956-171E-444	Sequence 444, App
6	146	14.7	11466	US-08-781-986A-444	Sequence 444, App
7	95.4	9.6	987	US-09-134-000C-838	Sequence 838, App
8	82.6	8.3	978	US-09-107-532A-366	Sequence 366, App
9	47.8	4.8	400	US-08-956-171E-3720	Sequence 3720, Ap
10	47.8	4.8	400	US-08-781-986A-3720	Sequence 3720, Ap
11	39	3.9	7218	US-08-232-463-14	Sequence 14, Appl
12	37.4	3.8	107140	US-09-949-016-14834	Sequence 14834, A
13	36.4	3.7	61663	US-09-453-702B-62	Sequence 62, Appl
14	36.4	3.7	61663	US-10-114-170-62	Sequence 62, Appl
15	34.4	3.5	4429	US-09-455-486-7	Sequence 7, Appl
16	34.2	3.4	2067	US-09-106-194-11	Sequence 11, Appl
17	34	3.4	505	US-08-621-576-15639	Sequence 15639, A
18	34	3.4	1083	US-09-134-000C-2381	Sequence 2381, Ap
19	33.4	3.3	295	US-09-313-294A-5605	Sequence 5605, Ap
20	33.2	3.3	872	US-09-270-767-25560	Sequence 25560, A
21	33.2	3.3	2228	US-09-270-767-10203	Sequence 10203, A
22	33.2	3.3	2460	US-08-952-365-1	Sequence 1, Appl
23	33.2	3.3	6065	US-09-800-729-35	Sequence 35, Appl
24	33.2	3.3	101011	US-09-949-016-16933	Sequence 16933, A

C 25	33	3.3	1801	3	US-08-669-304-30	Sequence 30, Appl
C 26	33	3.3	1801	3	US-09-824-053-30	Sequence 30, Appl
C 27	33	3.3	247299	3	US-09-949-016-17590	Sequence 17590, A
C 28	32.6	3.3	1200	3	US-09-107-532A-19	Sequence 19, Appl
C 29	32.6	3.3	1509	3	US-09-248-796A-3224	Sequence 3224, Ap
C 30	32.4	3.3	601	3	US-09-949-016-113423	Sequence 113423, A
C 31	32.4	3.3	601	3	US-09-949-016-163399	Sequence 163399, A
C 32	32.4	3.3	601	3	US-09-949-016-163400	Sequence 163400, A
C 33	32.4	3.3	601	3	US-09-949-016-163401	Sequence 163401, A
C 34	32.4	3.3	1340	3	US-08-956-171E-245	Sequence 245, App
C 35	32.4	3.3	1340	3	US-08-781-986A-245	Sequence 245, App
C 36	32.4	3.3	85869	3	US-09-949-016-12017	Sequence 12017, A
C 37	32.4	3.3	85878	3	US-09-949-016-16321	Sequence 16321, A
C 38	32.4	3.3	167708	3	US-09-949-016-16423	Sequence 16423, A
C 39	32.4	3.3	285986	3	US-09-949-016-12287	Sequence 12287, A
C 40	32.4	3.3	288031	3	US-09-949-016-14864	Sequence 14864, A
C 41	32.2	3.2	832	3	US-09-621-976-2813	Sequence 2813, Ap
C 42	32.2	3.2	255679	3	US-09-949-016-17189	Sequence 17189, A
C 43	32.2	3.2	786431	3	US-09-751-389-3	Sequence 3, Appl
C 44	32	3.2	870	3	US-09-543-681A-3984	Sequence 3984, Ap
C 45	32	3.2	930	4	US-09-605-703B-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-710-279-413
Sequence 413, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/09/710, 279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164, 258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 413
LENGTH: 990
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-09-710-279-413

Query Match 16.0%; Score 159; DB 3; Length 990;
Best local similarity 49.8%; Pred. No. 1.4e-39;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
QY 2 ATATGTCACAACTTTCATTTGAAATCTGACCGTAAACATGATTAGCAAGAA 61
8 ATATGTCACAACTTTCATTTGAAATCTGACCGTAAACATGATTAGCAAGAA 67
DB 62 TGAATTTTCATTTTCAGCGGAGACAGAGTATTTCTATCCGCCCGTTACAGTCGA 121
68 TGAATTTTCATTTTCAGCGGAGACAGAGTATTTCTATCCGCCCGTTACAGTCGA 127
QY 122 ACAGTAGACCTGACGAGAGGCGCCATCAGACAGTACGCGTTATCGTAGGAGAA 181
128 AATTGATCTAAGTTAGACAGCGCTT---GAATATGTTTGTGGAACAAATTAA 184
DB 182 AACTTGAAATATTTATTTTCCGACGCGATTTATGAAAGCGTTATCTTGCGGCGC 241
185 AAGTAGAGAGCTATATGATTTGATGATGATTAACAAAAGGTTAGCTATTTCAACC 244
QY 242 TTTATTTTCCGGGCTATGAGAGTACGAAAGAAAGATAGCGGAATACCGTTACATTTG 301
245 ATTACTTACTGTGTAGAGCTCTATACAGTACCATTAACGTTATGTTATTTAACTTAA 304

302 TCCGCGAAGAGTTTGTGACATGCGTGTCTGAGTCTGTGACGCTTTGGAAAGCGTAAAG 361
 305 CACCTGAGGAGATTATTGTGTGGGTTTAAAGGTTTAAATPAAAGTATTAGCGAATTTAAAC 364
 362 AAAAGATTGCATCTTTAACGATTTGAGAAAAAATAGANTCTATTGGATACAGTTTAC 421
 365 AAAAGGTTAAGAAATCAATATTATGATGATGAAAAAATACGACTTTGAATATCGTTCTC 424
 422 CGCTTCACTGATATTGTTCAGACCGGACGGGCCGAAACCTGACGATTAAGAACCAAGAC 481
 425 CTTTACATTTCAATGCTGACATGATGAAACAGGACATACCGTACCATAGAACCTCAAAATG 484
 482 ACGGCGCTCAAAAGTCTATGATTAATCAACCTGTGTGATGACGAACGCCCGCACTTAAAT 541
 485 GCTTATTATATGTTAAAGATATATTATGTTCAATCCTTAACAAATGAACTGAATTAAGATT 544
 542 GGCATGTATCAATCTGACGACATATTACAGAAATCAGACCGAAGCAATTAGAGACAAAG 601
 545 GGCATCTATCTTAACTTAAAGAAATTAACGCTTTTAAACGCACAGAAATCAACCAATCAAT 604
 602 AGATGGCGGAGATTAGCCCTTCTGCTTTGGCCAAAGGCTTAGAACTGTGTGCTGCCG 661
 605 TAATATGTAAGTCTGATTAAGATCAATGGCTGTGGAAGCAAAATGGCTTACCG 664
 662 GGGATTATACACCGCTTCCGGTTGTGACAGCTGTATTATTGAAAGAACATCTAAGAC 721
 665 GTGGTTATACGTCACAGATCGTTTAAATCGCGTACATATTAAAGACCAACCAATACGCT 724
 722 CGGCGCGCCGATGAAGAAAGGATTAACAGCGGCTTTTCAATTTTGGCAATATGACGA 781
 725 GTTCCCATTAAGAAATGAATTAATTAATGATTTTAAAGTTCTTAGAATACATGACGTA 784
 782 TACCAAGAGGCGCAGTGTATTAACGAAGAGAAAGCAATTCATTATACGCAATTAATCTCG 841
 785 TCCCTCAAGGTGCACTTAT--CGATGCCAATTAATATACATTAACACAAATATCATATTG 841
 842 TGATGTGCAAGAACTGGAATCTATTTCACACACATATGACAAATCGGCAATCCAA 901
 842 TGATGGAAGTAAAGAAAGAAAGTTATTATTAAGCTTACTTATGCAATCAAAATTTTCA 901
 902 AAGTAAATTTATTTCATGA 920
 902 AAATTAATTAATCAAGAGA 920
 RESULT 2
 US-09-134-001C-2421
 : Sequence 2421, Application US/09134001C
 : Patent No. 6380370
 : GENERAL INFORMATION:
 : APPLICANT: Lynn Doucette-Stamm et al
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 : FILE REFERENCE: GTC-007
 : CURRENT APPLICATION NUMBER: US/09/134,001C
 : PRIOR FILING DATE: 1997-11-08
 : PRIOR APPLICATION NUMBER: US 60/064,964
 : PRIOR FILING DATE: 1997-08-14
 : NUMBER OF SEQ ID NOS: 5674
 : SEQ ID NO 2421
 : LENGTH: 996
 : TYPE: DNA
 : ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-2421

Query Match	16.0%	Score 159	DB 3	Length 996
Best Local Similarity	49.8%	Pred. No. 1.4e-39		
Matches 458	Conservative	0	Mismatches 455	Indels 6
			Gaps 2	

QY 2 ATATGTGCACAGTCTTACATTGGAACTGCTGACCGTAAACATGTATTGCAAGAACAA 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	14	ATATGTGACGCGCATTTCTTTATATACAAAACAACGTTACCATATATTAGCTAGAACAA	73
QY	62	TGATATTTGCATTTCACTGGGGGACAGAGGTATCTCTATCCGGCGGTTACAGCTGGA	121
Db	74	TGACCTTTGCATTTGAATTTAATGATATCCAAACCATGTGTCACGCCATATACATACC	133
QY	122	ACAGTGAAGCTGACGGAAGGGCCCATCAGACACATGACGCGTTTATCGGTATGGGAGNA	181
Db	134	AATTGATCTAGATTTTCAGACATGGTGCTT---GATATGGTTTTGTGGAACAAAATTAA	190
QY	182	AACTTGGAATATATATTATTTGCCGACGGCATTTATGAAAAGCGGTTTATCTTGTGGCCG	241
Db	191	AAGTAGGACGTTATAGATTGTGTATGGTATPAACGAAAAGGTTTAGCTATTTGGAACC	250
QY	242	TTTATTTTTCCGGGCTATCGGAGTAGACGAAAACATACGGGAAAGATACCTGTTCATTTG	301
Db	251	ATTACTTCACTGCGTGAAGGCTCATACAGTACCACATTAACGTTATGTTATTTTACTTNG	310
QY	302	TCCCGCATGATTTGTGCATGGGCTGTCACTGTCTGCAGTCTTTGGAAAGCTPAAG	361
Db	311	CACCTGAGGAGTTTATGTGTGGGTTTATGGTTTAAAPAAAGTATAGCGAATTPAAAAC	370
QY	362	AAAGATTCGATCTTTAACGATTTGAGAGAAAATTTGATCTATTTGATACAGTTTAC	421
Db	371	AAAGGTTAAGAAATCAATTTATGATGATGAAAAAATACGACTTTGAAATATCGTTCCGC	430
QY	422	CGCTTCACTGATATTTGTCAAGCCGGAACGGGCCGAAACCTGACGATPAAGAACAGACAG	481
Db	431	CTTTACATTTTCATGGTCACTGATGAAACAGAACATACGTTAGCCATTAGAACCTTCAAAAG	490
QY	482	ACGGCCTCAAGTCTATGATATATCAACCTGGTGATGATACGAAACAGCCCCGACTTATAT	541
Db	491	GCTTATTAATGTGTAAGATATATTTATTTGTTCAATCTTAAACAATGAACTTAATTTAGAT	550
QY	542	GGCATGTATACCAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTTAGAGGCAAG	601
Db	551	GGCATCTATCTAATCTTAGAAATTAACGTTTTTTTAACGCCACAGAAATCAACCAATCAAT	610
QY	602	AGATGGCGGATTAACCCCTTCTGTGCTTTTGGCAGGCGTTAGGAATGTTGGCTTCGCCG	661
Db	611	TAAATGTGTAAGTGTCTAGTAAGATCAATGGGCTGTGAACAGGAAACAAATGGCTTACCG	670
QY	662	GGGATTAATACACCGGCTTCCGGTGTTCAGAGCTGTTATTTGAAAGAACATCTAGAGC	721
Db	671	GTGTTATACGTCACAACAGATGTTTATTAACGGCTCAATATTTAGACACCAACTACGCT	730
QY	722	CGGCGGCGGATGAAAAGAAAGGTGTACAGCCGCTTTTCAAAATTTGGCAATATGACGA	781
Db	731	GTTCCTCATATGAAATGATAAAATTTAAAGAAATTTGTTTTAAAGTTCTAGATCAGTACGA	790
QY	782	TACCAAAAGGGCGGAGTGAATACGGAAGAAAGAAATTCATTAATCGCAATATATCTTCG	841
Db	791	TCCCTCAAGGTGCACTAT--CGATGCCAATPAATATCATTTACACACATATCATTAG	847
QY	842	TGATGTGCACGAAACGTAACCTATATTTCCACACATATGACAAATCGGCAATCCAA	901
Db	848	TGATGAAAGTAAAGAAAGAAAGTATTTATTAAGCCTTACTTAGCAATCAAAATTTTCA	907
QY	902	AAGTAAATTTATTTCAATGA 920	
Db	908	AAATTAATTAATCTGAAGA 926	

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3 RESULT 3
US-09-710-279-3345/C
/ Sequence 3345, Application US/09710279
/ Patent No. 6703492
/
/ GENERAL INFORMATION:
/ APPLICANT: KIMBERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: pm3480US
/ CURRENT APPLICATION NUMBER: US/09/710.279
/ CURRENT FILING DATE: 2000-11-09
/

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PRIOR APPLICATION NUMBER: 60/164,258
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3345
 LENGTH: 2975
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: nucleic acid sequence
 US-09-710-279-3345

Query Match 16.0%; Score 159; DB 3; Length 2975;
 Best Local Similarity 49.8%; Pred. No. 2.5e-39;
 Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTCACAAGCTTACATTTGGAACCTGACCTTAACATGTATTAGCAAGAACAA 61
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 DB 1755 ATATGTCACAAGCTTACATTTGGAACCTTAACATGTATTAGCAAGAACAA 1696
 62 TGGATTTTGCATTTAGCTGGGACAGAGGTGATTCCTATCCGCGCGCTTACAGCTGA 121
 1695 TGGACTTTGATTTGATTTAATGTATCCCAACCAATTTCCACGCCATTATCATTACC 1636
 QY 122 ACAGTGAAGCTGACGGAAGGCCCATCAGACAGTACCGGTTATCGGTATGGGAGAA 181
 1635 AATTGATCTAGATTCAGATCAGATCGCTT---GAATATGGTTTGTGGAAACAAATTAA 1579
 DB 182 AACTTGAATAATATTATTGCGGACGCGCTTATGAAACGGTTATCTTGGCGCGC 241
 1578 AAGTAGAGCTATTAAGATTTGTGATGTATTAACGAAAAAGGTTAGCTATTTGCAACC 1519
 QY 242 TTATTTTCCGGCTATGCGAGTACGAAAAAAGATACGGAAGATACCGTTACATTG 301
 1518 ATTACTTCACTGTGAGAGCTCATACGATCCATTAACCTTATGTATTATTACCTAG 1459
 DB 302 TCCCGCATAGTTTGTGACATGGGTCTGTCACTGTGCTGATCTTTGGAAGACGTAAAG 361
 1458 CACCTGAGAGTTTATTTGGTTTGGTTTAAAGATTAAGATTAAGCAATTAAC 1399
 QY 362 AAAAGATTGATTTTAAGATTTGTAGAGAAAAAATTAATGATCTATGATACGATTTC 421
 1398 AAAAGTTAAGAAAAATCAATATTATGATGAAAAAATACGATTTGAATATGTTCTC 1339
 DB 422 CGCTTCACTGATATTGTGACAGCGGCGGAAACCTGACGATGAACCAAGACAG 481
 1338 CTTTACATTTCATGTCATGATGAAACAGACATACCGTACGATGAACTCACAATG 1279
 QY 482 ACGGCTCAAGTCTATGATATCAACCTGTGTCTATGACGAACAGCCCGACTTATAT 541
 1278 GCTTATTAATAGTAAAGATTAATATGTTTCACTTAACTTAACAAATGAACCTTAATGAT 1219
 DB 542 GGCATGTAACCAATCTGACGCAATATACAGAAATCAAGCGAAACATTTAGAGCAAG 601
 1218 GGCATGTAACCAATCTTAAAGAAATACGCTTTTAAACGCAAGAAATCAACCAATCAAT 1159
 QY 602 AAGATGGCGGATTAAGCCCTTTCCTTTGGCCAAAGCTTAAGGACGTTGTGTGCGCG 661
 1158 TAAATAGTAAAGTCTAGTAAATCAATGGGCTGTGAGAGCAAGAAATAGGCTTACCG 1099
 DB 662 GGGATTATACACCGCTTCCCGGTTTGTCAAGCTCTTTATTTGAAGAATCATCTAGAC 721
 1098 GTGGTATATAGTCAACAGATCGTTTATAGCGCTACATATTTAAGACCAACCTACGCT 1039
 QY 722 CGGCGGCGCATGAAGAAAGGTGTAACAGCGCTTTTCAAAATTTGGCAAAATATACGA 781
 1038 GTTCCATATATGAAGTGAAGATTTAATGATTTTAAAGTTCTAGAAATCAGTACGTA 979
 DB 782 TACCAAGGCGCATGATACGGAAGAGACGAATTTCAATTACGCAATATACCTTCCG 841
 978 TCCCTCAAGGTGCAATTA---CGATGCCAATTAATATCACTTACACAAATATCAATTAG 922

QY 842 TGATGTCACGAACTGAAACTACTATTTCACCATATATGACAAATCGGCAATCCAA 901
 |||||
 DB 921 TGATGAAAGTAAAGAAAGATTAATATATTAAGCTTACTTACGATCAATATTTC 862
 QY 902 AACTAATTTATTTCTATGA 920
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 DB 861 AATTAATAATTAAGTGAAG 843

RESULT 4 US-09-710-279-4184

; Sequence 4184, Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMBERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: P03480US
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4184
 ; LENGTH: 4114
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-09-710-279-4184

Query Match 16.0%; Score 159; DB 3; Length 4114;
 Best Local Similarity 49.8%; Pred. No. 2.9e-39;
 Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTCACAAGCTTACATTTGGAACCTGACCTTAACATGTATTAGCAAGAACAA 61
 |||||
 DB 1626 ATATGTCACAAGCTTACATTTGGAACCTTAACATGTATTAGCAAGAACAA 1685
 62 TGGATTTTGCATTTAGCTGGGACAGAGGTGATTCCTATCCGCGCGCTTACAGCTGA 121
 1686 TGGACTTTGATTTGATTTAATGTATCCCAACCAATTTCCACGCCATTATCATTACC 1745
 QY 122 ACAGTGAAGCTGACGGAAGGCCCATCAGACAGTACCGGTTATCGGTATGGGAGAA 181
 1746 AATTGATCTAGATTCAGATCGCTT---GAATATGGTTTGTGGAAACAAATTAA 1802
 DB 182 AACTGGAATAATATTATTGCGGACGCGATTAAAGAAAGGTTATCTTGTGCGCGC 241
 1803 AAGTAGAGCTATTAAGATTTGTGATGTATTAACGAAAAAGGTTAGCTATTTGCAAC 1862
 QY 242 TTTATTTTCCGGCTATGCGAGTACGAAAAAAGATACGGAAGATACCGTTACATTG 301
 1863 ATTACTTCACTGTGAGAGCTCATACGATCCATTAAGGTTATGTTTAATTTAACTTGA 1922
 DB 302 TCCCGCATAGTTTGTGACATGGGTCTGTCACTGTGCTGATCTTTGGAAGACGTAAAG 361
 1923 CACCTGAGAGTTTATTTGGTTTAAAGTTTAAATTAAGTATTAGCAATTTAAAC 1982
 QY 362 AAAAGATTGATCTTTAAGATTTGAGAAAAAATTAAGATCTATTTGATACGTTTAC 421
 1983 AAAAGTTAAGAAAAATCAATATTATGAAATGAAAAAAATACGATTTGAATATGTTCTC 2042
 DB 422 CGCTTCACTGATATTGTGACAGCGGCGGAAACCTGACGATGATGAACCAAGACAG 481
 2043 CTTTACATTTCACTGATGTAAGCAAGACATACCGTACGATGATGATGATGATGATG 2102
 QY 482 ACGGCTCAAGTCTATGATATCAACCTGTGTGATGACGAACAGCCCGACTTATAT 541
 2103 GCTTATTAATAGTAAAGATTAATATGTTTCACTTAAAGATTAAGTAAATTAATGAT 2162
 DB 542 GGCATGTAACCAATCTGACGCAATATACAGATCAACGGAAGCAATTAAGAGCAAG 601

OY 964 GAAGAGTATTCATGACCTTAATTA 989
DB 2731 CATATCACTATTAGAAAGTTGAATGA 2706

RESULT 6

US-08-781-986A-444/C
; Sequence 444, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11466 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-444

Query Match 14.7%; Score 146; DB 3; Length 11466;
Best Local Similarity 47.5%; Pred. No. 6,3e-35;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

OY 4 ATGTGCAAGTCTTACATTTGAAACTGACCGTAAACATGTATTAGCAAGAACATG 63
DB 3688 ATGTGCAAGTCTTACATTTGAAACTGACCGTAAACATGTATTAGCAAGAACATG 3629
OY 64 GATTTCGATTCAGCTGGGGAACAGAGTATCTTATCCGCGCTTACAGCTGAGAC 123
DB 3628 GATTTCGATTCAGCTGGGGAACAGAGTATCTTATCCGCGCTTACAGCTGAGAC 3569
OY 124 AGTGAAGCTGACGGAAGGCGCCATCAGACAGTACCGCTTATTCGCTATGGGAGAAA 183
DB 3568 TCTTGCACT--GCAACGAGAGGCGCAACGCAATATGCTTTATGGCAGAGAAACGAT 3512
OY 184 CTGGAATATATATATTTGCGGACGCGCATTAATGAAGCGTTATCTTGCGCGGCTT 243
DB 3511 ATGGAAGTATTTATTTATGCTGATGATGATTAATGAAGATGCGCTTGCAATTCACAA 3452
OY 244 TATTTTCGGGCTATGCGAGTACGAAAAAGATACGGAAGATACCGTTCACTTGC 303
DB 3451 TATTTTCGGGCTATGCGAGTATGCTATGATCAACACACAAACGAGCGATGAATATTACG 3392
OY 304 CGCATGAGTTTGTGACATGGGCTGCTCAGTCTGTCAGCTTTGGAAGCGTAAAGAA 363

DB 3391 CAAATGAAATTTGACATGATTTTGGATATACAAACAGCATTTGAAGATATGAAACA 3332
OY 364 AAGATTCATCTTTAAGATTTAGAGAAAAATATGATCATATGATGATTAACCG 423
DB 3331 CAGCATCCCAATATCATGTTGTAGCTGTATTTATTTAATGACATCGGTGAAGTCCGCA 3272
OY 424 CTTCATGATATTTGTCAGACCGGACCGGCGAAACCTGACGATGAAACCAAGACAC 483
DB 3271 TTGCATATCATGTTTCCGATGCACTGACATATGATCGAAGTTTCAATTAAGAGGGT 3212
OY 484 GGCTCAATCTATATATATCAACCTGTGTATGACGACACCGCCGATTTATATG 543
DB 3211 GAAGTGTATTAAGAGTAACTCTATGGTGTCTTAAATCAATCATCAAGCTTAAATGG 3152
OY 544 CATGTAACTCTGACGATATATACAGAAATGACGACGAAACATTTAGAGCAAAAG 603
DB 3151 CATTTATGTATTTAAGACATATATATATTTCTCTTATCCAGCAACGAAATTTA 3092
OY 604 ATGGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTAAAGCTGTGCTGCGGG 663
DB 3091 TTGGAAGGTGTAACATTTAAACCTTTAGGCAATGAGCAGTACATTTGATTCAGGT 3032
OY 664 GATTATACACCGCTTCCCGCTTTGTCAGAGCTGTTATTTGAAAGAACTTACAGCC 723
DB 3031 GAATTAATCTTCACTGACGCTTTGAGATGCAATTTATGAAAGCAATTCCTCAA 2972
OY 724 GCGGCGGATGAAGAAAGGTATGACGCGCTTTCAATTTTGGCAATATGACGATA 783
DB 2971 AACATATATTAAGAAATGATTTAATGATGATCTTTATTTATGATGCGGTAAATTA 2912
OY 784 CCAAGGCGCAGTGTATTAACGAAAGAAAGCAAAATCATTTATGCAATATCTCCGT 843
DB 2911 CCGATTTGATTTGATGCTGCGATGATGCTGACAAATCAGATATGATGACAGCGTA 2852
OY 844 ATGTGCAAGAACTGGAATCTATTTTCCACCATATGACATCGCAATTCGAAATA 903
DB 2851 ATTAATTTAATCTAAGAAAGTATATATTAATGATATATGACGATGATTAATGCA 2792
OY 904 GTAATTTATTTATGAAAGCTTGAATGTTGAGGCTTAAAGTGTTCGCTAAAGCA 963
DB 2791 TTTAAGCTCAGATATATTTAATTAAGAAAGATATGACATTTTAAAGCTGAGAG 2732
OY 964 GAAGAGATATTCATGACCTTAATTA 989
DB 2731 CATATCACTATTAGAAAGTTGAATGA 2706

RESULT 7

US-09-134-000C-838
; Sequence 838, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 838
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-838

Query Match 9.6%; Score 95.4; DB 3; Length 987;
Best Local Similarity 45.8%; Pred. No. 1.6e-19;
Matches 407; Conservative 0; Mismatches 476; Indels 6; Gaps 2;

OY 41 AACATGATTAACAAAGAACATGATTTTGCATTTCACTGGGAGCAGAGGTGATTTCTCT 100

Db 605 GTTGAATGCTTATAGCCGCGTATGGAGGATAGGGTTCCTGGAATTTATCTCAG 664
Qy 677 CTTCCTCGGTTTGTGACAGCTGTTTATTTGAAGAATCTAGAGCCGGCGCATTA 736
Db 665 TATCTCGTTTGTATTAACGACTTTTACGAGCTGATTCGTATCTGAGATTCAAGT 724
Qy 737 CGAAGGTGTAACGCCGCTTTTCAATTTTGGCAATATGACATACCAAGGCGCAG 796
Db 725 CAGAAAGTATAGCAATTTTCCATCTTAGGTTGAGAACAAACAAAGGTTGT 784
Qy 797 TGAATAGGAGAGACGAATATCATTTATAGCAATATCTCGTATGACAGAA 856
Db 785 GTGATGTTGTGAAGAAATATGAAATATGCAATTTATCTTGTGCAATGTTGCA 844
Qy 857 CTGGAATCTATTTCCACCATATGACATCGCAATCCAAATTAATTTATTC 916
Db 845 AAGGATATATATATATGAAACATATGAAACAGTCAATTTACTGCAATTTATGAATA 904
Qy 917 ATGAAGACTTGAAGTTTGAAGCCTTAAGTGTTCGCTTAAGCAGAGATATTC 976
Db 905 AAGAGCTTGAATGATGATATGATTAATGATATCCATATATGAAAAACAAATTA 964
Qy 977 ATGAGCTTAATTA 989
Db 965 AATATATTAATTA 977

RESULT 9

US-08-956-171E-3720/C

Sequence 3720, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 3720:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
US-08-956-171E-3720

Query Match 4.8%; Score 47.8; DB 3; Length 400;
Best Local Similarity 48.1%; Pred. No. 0.0001;
Matches 136; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

Qy 286 GATACCGTCAATTCGCCGATGAGTTTGTGACAGGGGCTGCTGAGTGTGACGCT 345
Db 333 GAGCGATGATATATTCAGCAAAATGATGACATGATTTGGATATACAAACAGC 274
Qy 346 TTGGAACCGTAAAGAAAGATTCGATCTTTAAGATTTAGAGAAATTAATGATCTA 405
Db 273 ATGAATATATGAAACAAAGACATCCCAATCATGTTAGCTGATATTTAATGAC 214
Qy 406 TTGATACAGTTTACCGCTTCACTGATATTTGTGACACCGGACGGCCGAACTGACG 465
Db 213 ATCGTGAAGTTCCGCGCATTCATATCATGTTTCCGATGCACTGACATACAGTCGAA 154
Qy 466 ATGAACCAAGAGACAGCGCTCAAGTCTATGATATGACCTGCTGATGACGAC 525
Db 153 GTTTCATTAAAGAGGTGAAGTGTATTAAGATATCTATTTGGTGTCTTAACAAT 94
Qy 526 AGCCCGACTTTATATGACATGTAACCATCTGACGACATATA 568
Db 93 CATCCAGACTTAATTTGGCATTTATGTAATTTAAGCAATATA 51

RESULT 10

US-08-781-986A-3720/C

Sequence 3720, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 3720:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-3720

Query Match 4.8%; Score 47.8; DB 3; Length 400;

Best Local Similarity 48.1%; Pred. No. 0.0001;
Matches 136; Conservative 0; Mismatches 147; Indels 0; Gaps 0.

QY	286	GATACCGTTCACTTGTCCCGCATGAGTTTGACATGAGGAGCGTCAGTCTGCACTCT	345
Db	333	GAGCCGATGAATTTACCCAAAATGAAATTGGACATGGATTTTGGGTAACAAACAAGC	274
QY	346	TTGGAGAAGCTAAAGAAAAGATTGCATCTTTAACGATTGAGAAAATTTGATCTA	405
Db	273	ATTGAAGATGTGAACAACAAGCATCCCAATACATGTTGAGCGTTATTTTAAATGAC	214
QY	406	TTGGATACAGTTTAAACGCTTCACTGATATTGTACAGCCGACGGCGCGAAACCTGACG	465
Db	213	ATGCGTCAGATTCCGCATTGCATTATCAATGTTTCGATGCACTGCAATACAGTGGAA	15
QY	466	ATAGAACCAAGACAGACGGCCTCAAAAGTCTATGATAATCAACCTGGTGTCAATAGCAAC	525
Db	153	GTTCATTTTAAAGAGGGGTGAAGTGTATTAAGAAAGTAATCCATATGGTGTCTTTAACAAT	94
QY	526	AGGCGGACCTTATATGACGATGAACCAATCGACGACATATA	568
Db	93	CATCCAGACTTAAATGGCATTTATAGTAATTTTAAGCAATATA	51

RESULT, 11

US-08-232-463-14/c
; Sequence 14, Application US/08232463

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F

APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 1
ADDRESS: 1

ADDRESSEE: Foley & Larnner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria

STATE: VA
CITY: Alexandria
COUNTRY: USA

COUNIK1: USA
ZIP: 22313-0299
COMPTON PERADARIT FORM:

COMPIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPIER: IBM PC compatible

[illegible]

COL NAME: INCHES: 10.000 11.000
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/08/2332 463

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313

FILING DATE: EP 91 114 300
APPLICATION NUMBER:

FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMUNO
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109

TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
;

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;          TOPOLOGY: linear
;
;          IMMEDIATE SOURCE:

```

CLONE: PTZgpt-F18
US-08-232-463-14

Query Match	3.9%;	Score 39;	DB 2;	Length 7218;
Best Local Similarity	5.8%;	Pred. No. 0.28;		
Matches 24;	Conservative 206;	Mismatches 181;	Indels 0;	Gaps 0

Oy		ACCTGAGATTAAGAAACCAAGAAGCACAAGCGCCCAAAGTCAATATATCAACTGGTCGA	517
Db		1436 ACRR	137
Oy		518 TGAAGAACAGCCCCGACTTATATATGCAATGTACCAATCTGACGAATATACAGAAATCA	577
Db		1376 RR	131
Oy		578 GACCGAAGCAATTYAGAGACAAAGAGATGGCGGATTAGCCCTTTCTGCTTTGGCCAG	637
Db		1316 RR	125
Oy		638 GTTAGAAGACTGGTGCTGCCTGGGGGATTATACACGCCCTTCCCGTTTGCAGAGCTG	697
Db		1256 RR	119
Oy		698 TTATATTGAAGAACATCTAGAGCGCGCGCGCATGAACAGAAAGTGTATACAGCCGCTT	757
Db		1196 RR	113
Oy		758 TTCAAATTTGGCAATATGACGATACCAAGGGCGCGATTAACGGAAGAAAGCA	817
Db		1136 RR	107
Oy		818 TTCAATTATAGCAATAATACTCCGATGTGCCAAGAACTGGAAACTACT	868
Db		1076 RRRRRRRRBATCCGAAGCTCCCTCGAAGCTGCAAGAGCTCGGAATTAAT	1026

RESULT 12

US-09-949-016-14834
; Sequence 14834, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH CERVICAL DYSPLASIA
 ; FIELD OF INVENTION: METHODS OF DETECTING
 ; AND PREVENTING CERVICAL DYSPLASIA

FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: 05/05/945,016
 ; CURRENT FILING DATE: 2000-04-14
 ; CURRENT PRIORITY NUMBER: 00/341 3EE

; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR APPLICATION NUMBER: 60/231,186
 ; PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231 488

; PRIOR APPLICATION NUMBER: 80/251,150
 ; PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 307013

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14834

```

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; SEQ ID NO 1003
;
; LENGTH: 107140
;
; TYPE: DNA

```

; FILE: DNA
 ; ORGANISM: Human
 ;
 HHS-09-949-016-14834

Query Match 3.8% Score 37.4

Best Local Similarity	49.7%;	Pred. No. 3.7;
Matches	95;	Conservative
Mismatches	96;	Indels
Gaps	0	

QY	682	CGGTTGTCAGAGCTGTTATTGAAAGACATCTAGACCCGGCCGATGAAACGAA	741
Db	3534	CGTTTGGGAGAGGTATATTTAAAAAAGGACAGAGGCGAOTCTTTAAAGAAAA	3539
QY	742	GGTGTAAACAGCCGCTTTTCAATTTTGGCAATATGACGATCCAAAGGCCGACGTATA	801
Db	3594	AGGGAACGAGGAATGTGTTTTCTGTAGAGGATACAGAAAGACCTGTGGGGTCTTT	3555
QY	802	ACGGAAGAAGACGAATTCATTATACGCAATATCTCCGTGATGTGCACAGCAATCTGA	861
Db	3654	GCCTAAGACATTTACCTTTGTAAACAGAAACCATCCCAATAACTCATTGATTTTTGT	3713

QY 862 AACTACTATT 872
DB 3714 AACTATTTT 3724

RESULT 13

US-09-453-702B-62/c

Sequence 62, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.

Burland, Valerie

Perna, Nicole T.

Plunkett, Guy

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-DEC-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 61663

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-09-453-702B-62

Query Match 3.7%; Score 36.4; DB 3; Length 61663;

Best Local Similarity 49.5%; Pred. No. 5.7;

Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 615 AGCCCTTCTGCTTTGGCGAAGCTTAGAAGCTTGTGCGCGGGGATTATACACC 674
DB 12338 AGCCCTTCTGCTTTGGCGAAGCTTGTGCGCGGGGATTATACACC 12879
QY 675 GCCTTCCCGGTTTGTCAAGCTGTTTATTTGAAGAATCATCTAGAGCGCGCGCGATGA 734
DB 12878 CTATCAAGATTGTGCAAGATATCTTTTGTAAGTCTTCACTAGTATTAAGTTGA 12819
QY 735 AAGCAAGGTTAAGACCGCTTTTCAATTTTGGCAATATGACGATACCAAGGCGCG 794
DB 12818 ACTGAAAGTTTGGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 12759
QY 795 AGTGATACG 804
DB 12758 AAGGAATTCG 12749

RESULT 14

US-10-114-170-62/c

Sequence 62, Application US/10114170

Patent No. 6855814

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.

Burland, Valerie

Perna, Nicole T.

Plunkett, Guy

TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-APR-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 61663

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-10-114-170-62

Query Match 3.7%; Score 36.4; DB 3; Length 61663;

Best Local Similarity 49.5%; Pred. No. 5.7;

Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 615 AGCCCTTCTGCTTTGGCGAAGCTTAGAAGCTTGTGCGCGGGGATTATACACC 674
DB 12338 AGCCCTTCTGCTTTGGCGAAGCTTGTGCGCGGGGATTATACACC 12879
QY 675 GCCTTCCCGGTTTGTCAAGCTGTTTATTTGAAGAATCATCTAGAGCGCGCGCGATGA 734
DB 12878 CTATCAAGATTGTGCAAGATATCTTTTGTAAGTCTTCACTAGTATTAAGTTGA 12819
QY 735 AAGCAAGGTTAAGACCGCTTTTCAATTTTGGCAATATGACGATACCAAGGCGCG 794
DB 12818 ACTGAAAGTTTGGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 12759
QY 795 AGTGATACG 804
DB 12758 AAGGAATTCG 12749

RESULT 15

US-09-455-486-7/c

; Sequence 7, Application US/09455486

; Patent No. 6833438

; GENERAL INFORMATION:

; APPLICANT: Daniel E. Afar

; APPLICANT: Rene S. Hubert

; APPLICANT: Arthur B. Raitano

; APPLICANT: Douglas C. Saffran

; APPLICANT: Stephen C. Mitchell

; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

; FILE REFERENCE: 129.17-US-11

; CURRENT APPLICATION NUMBER: US/09/455,486

; PRIOR FILING DATE: 1999-12-06

; PRIOR FILING DATE: 1999-06-01

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 4429

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (85)...(1464)

US-09-455-486-7

Query Match

Best Local Similarity 3.5%; Score 34.4; DB 3; Length 4429;

Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY	243	TTATTTCCGGGCTATCGGAGTACGAAACGATACGGGAAGATACCGTTCACATTTGT	302
DB	1726	TCATCTCAGCTCCTCAGGCTCTCGGAAATAGAGTCAGGACCTGACTGATTTCTCA	1667
QY	303	CCGCGATGAGTTGTGACATGGGTGCTGTCAGTCTGTCAGTCTTTGGAGACGTAAAGA	362
DB	1666	CTAACCTGAGATTAATAGTGTCTCTTCAGTATGTCAGTCAATTTCTCAAGACACAGC	1607
QY	363	AAAGATTGATCTTTAAGCATGTAGAGAAAAATT	398
DB	1606	AATGTTTCCTCAGTCACGGGTGTAAGAAAAAACTT	1571

Search completed: March 18, 2006, 11:58:33
Job time : 228 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:52:29, Search time 992 Seconds
(without alignments)
8302.722 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996
Sequence: 1 catatgcgcacagctctac.....atgagcttaattagatcc 996

Scoring table:
IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	996	US-10-812-387-1	Sequence 1, Appli
2	439.8	44.2	990	US-09-974-300-1719	Sequence 1719, Ap
3	287.8	28.9	984	US-10-282-122A-9120	Sequence 9120, Ap
4	237	23.8	969	US-10-282-122A-9817	Sequence 9817, Ap
5	232.6	23.4	990	US-10-398-221-766	Sequence 766, App
6	232.6	23.4	990	US-10-398-221-2682	Sequence 2682, Ap
7	232.6	23.4	990	US-10-282-122A-24755	Sequence 24755, A
8	173.8	17.4	1616	US-10-429-802-17	Sequence 17, Appli
9	173.8	17.4	1616	US-10-430-503-8	Sequence 8, Appli
10	160.2	16.1	978	US-10-282-122A-34300	Sequence 34300, A
11	159	16.0	996	US-10-724-972A-1455	Sequence 1455, Ap
12	146	14.7	993	US-10-282-122A-7960	Sequence 7960, Ap
13	146	14.7	11466	US-08-781-986A-444	Sequence 444, App
14	146	14.7	11466	US-10-329-624-444	Sequence 444, App
15	142.4	14.3	1002	US-09-815-242-8383	Sequence 8383, Ap
16	142.4	14.3	981	US-09-815-242-4665	Sequence 4665, Ap
17	117.8	11.8	972	US-10-282-122A-35759	Sequence 35759, A
18	95.4	9.6	972	US-10-282-122A-20906	Sequence 20906, A
19	80.6	8.1	972	US-10-282-122A-21716	Sequence 21716, A
20	80.2	8.1	2256646	US-10-470-565-1	Sequence 1, Appli
21	72.4	7.3	1050	US-10-282-122A-12199	Sequence 12199, A
22	63.6	6.4	978	US-10-398-221-911	Sequence 911, App
23	63.6	6.4	978	US-10-398-221-2826	Sequence 2826, App

24	61.8	6.2	579	7	US-10-282-122A-21539	Sequence 21539, A
25	55.2	5.5	1092	7	US-10-282-122A-40070	Sequence 40070, A
26	53.6	5.4	1092	7	US-10-282-122A-38691	Sequence 38691, A
27	52.2	5.2	9749	7	US-09-070-927A-154	Sequence 154, App
28	47.8	4.8	400	2	US-08-781-986A-3720	Sequence 3720, Ap
29	47.8	4.8	400	7	US-10-329-624-3720	Sequence 3720, Ap
30	40.8	4.1	37973	6	US-10-311-465-2169	Sequence 2169, Ap
31	37.2	3.7	1068	3	US-09-815-242-6788	Sequence 6788, Ap
32	37	3.7	10528	6	US-10-311-465-307	Sequence 307, App
33	36.4	3.7	61663	6	US-10-418-837-1	Sequence 1, Appli
34	36.4	3.7	61663	5	US-10-114-170-62	Sequence 62, Appli
35	36	3.6	826	3	US-09-070-927A-799	Sequence 799, App
36	35.8	3.6	583	4	US-09-925-065A-392869	Sequence 392869, A
37	35.8	3.6	3673778	6	US-10-312-841-2	Sequence 2, Appli
38	35.4	3.6	245	3	US-09-880-107-1689	Sequence 1689, App
39	35.4	3.6	419	4	US-09-925-065A-654182	Sequence 654182, A
40	35.4	3.6	419	4	US-09-925-065A-654183	Sequence 654183, A
41	35	3.5	600	9	US-10-972-079-44650	Sequence 44650, A
42	35	3.5	661	7	US-10-648-553-102	Sequence 102, App
43	35	3.5	1053	9	US-10-450-763-28412	Sequence 28412, A
44	35	3.5	11036	5	US-10-239-676-118	Sequence 118, App
45	35	3.5	11036	6	US-10-240-453-138	Sequence 138, App

ALIGNMENTS

RESULT 1	US-10-812-387-1	US-10-812-387-1
Sequence 1, Application US/10812387		
Publication No. US20050142652A1		
GENERAL INFORMATION:		
APPLICANT: SIVARAMAN, HEPHIZIBAH		
APPLICANT: PUNDLE, ARCHANA VISHNU		
APPLICANT: SURESH, CHEERAVAKATTU GOPALAN		
APPLICANT: DODSON, GEORGE GUY		
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF LARGE AMOUNT OF PENICILLIN V		
TITLE OF INVENTION: ACYLASE		
FILE REFERENCE: 056859-0196		
CURRENT APPLICATION NUMBER: US/10/812.387		
CURRENT FILING DATE: 2004-03-30		
PRIOR APPLICATION NUMBER: PCT/IB03/06198		
PRIOR FILING DATE: 2003-12-24		
NUMBER OF SEQ ID NOS: 1		
SOFTWARE: PatentIn Ver. 3.2		
SEQ ID NO 1		
LENGTH: 996		
TYPE: DNA		
ORGANISM: Bacillus subtilis		
US-10-812-387-1		
Query Match	100.0%;	Score 996; DB 9; Length 996;
Best Local Similarity	100.0%;	Pred. No. 1.6e-289;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
1	CATATGTCACAGTCTTACATTTGGAAGCTGACCGTAAATGATTTAGCAAGACA	60
1	CATATGTCACAGTCTTACATTTGGAAGCTGACCGTAAATGATTTAGCAAGACA	60
61	ATGAGATTTGCAATTCAGCTGAGGACAGAGGTATTTCTATCCGCGCTTACAGCTGG	120
61	ATGAGATTTGCAATTCAGCTGAGGACAGAGGTATTTCTATCCGCGCTTACAGCTGG	120
121	AACAGTGAAGCTGACGGAAGGCGCCATCAGACAGTACCGCTTATCGGTATGGGAGCA	180
121	AACAGTGAAGCTGACGGAAGGCGCCATCAGACAGTACCGCTTATCGGTATGGGAGCA	180
181	AAACTGGAATATATTTATTTGCGGACGCGATTAATGAAGCGGTTATCTTGCGGCG	240
181	AAACTGGAATATATTTATTTGCGGACGCGATTAATGAAGCGGTTATCTTGCGGCG	240
241	CTTATTTTCCGGGCTATGCGAGTACGAAAAAGATACGGGAGATACCGTTCACTT	300

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Db      241 CTTTATTTTCGGGCGATCGAGTACGAAAAACATACGGGAATACCGTTACATT 300
Qy      301 GTCCGCATGAGTTTGTGACATGGGTCTGTCACTGTCTGTCAGTCTTTGGAAGCTTAAA 360
Db      301 GTCCGCATGAGTTTGTGACATGGGTCTGTCACTGTCTGTCAGTCTTTGGAAGCTTAAA 360
Qy      361 GAAAGATTCGATCTTTAAGATTTAGAGAAAAATTTGATCTATTTGATCAGTTTA 420
Db      361 GAAAGATTCGATCTTTAAGATTTAGAGAAAAATTTGATCTATTTGATCAGTTTA 420
Qy      421 CCGCTTCACTGATATTTGTCAAGCCGACCGGCGGAACTTGAAGTAGAACCAAGACA 480
Db      421 CCGCTTCACTGATATTTGTCAAGCCGACCGGCGGAACTTGAAGTAGAACCAAGACA 480
Qy      481 GACGCGCTCAAAAGTCTATGATTAATCAACTGTGTGTCAAGACGACCCCGACTTATA 540
Db      481 GACGCGCTCAAAAGTCTATGATTAATCAACTGTGTGTCAAGACGACCCCGACTTATA 540
Qy      541 TGGCATGTAAACCAATCTGACAGCAATTAACAGAAATCAACGCAATTAGAGACAAA 600
Db      541 TGGCATGTAAACCAATCTGACAGCAATTAACAGAAATCAACGCAATTAGAGACAAA 600
Qy      601 GAGATGGCGGATTAACCCCTTCTGCTTTTGGCCAAAGCTTAGAACTGTGTGCTGCCG 660
Db      601 GAGATGGCGGATTAACCCCTTCTGCTTTTGGCCAAAGCTTAGAACTGTGTGCTGCCG 660
Qy      661 GGGGATTTATACCGGCTTCCCGGTTTGTCAAGCTGTTATTTGAAAGCACTTAGAG 720
Db      661 GGGGATTTATACCGGCTTCCCGGTTTGTCAAGCTGTTATTTGAAAGCACTTAGAG 720
Qy      721 CCGGCGGCGGATTAACGAAAGGTTTACAGCCGCTTTCAAAATTTGGCAATATAGAG 780
Db      721 CCGGCGGCGGATTAACGAAAGGTTTACAGCCGCTTTCAAAATTTGGCAATATAGAG 780
Qy      781 ATACCAAAAGGCGCAGTATGATACGAGAAAGCAAAATTCATTATACGAAATATCTCC 840
Db      781 ATACCAAAAGGCGCAGTATGATACGAGAAAGCAAAATTCATTATACGAAATATCTCC 840
Qy      841 GTGATGTGCAACGAACTGAAATCTATTTCCACACATATGACAAATCGGCAATTCGA 900
Db      841 GTGATGTGCAACGAACTGAAATCTATTTCCACACATATGACAAATCGGCAATTCGA 900
Qy      901 AAGTAAATTTATTTCAAGAACTTGAAGCTTGAAGCTTAAAGTCTTTCCGCTAAA 960
Db      901 AAGTAAATTTATTTCAAGAACTTGAAGCTTGAAGCTTAAAGTCTTTCCGCTAAA 960
Qy      961 GCAGAGAGATTCATGAGCTTAATTAAGATCC 996
Db      961 GCAGAGAGATTCATGAGCTTAATTAAGATCC 996

RESULT 2
US-09-974-300-1719
; Sequence 1719, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 1085, 500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1719
; LENGTH: 990
; TYPE: DNA

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; ORGANISM: Bacillus licheniformis
US-09-974-300-1719
Query Match      44.2%   Score 439.8; DB 3; Length 990;
Best Local Similarity 65.3%; Pred. No. 1,5e-121;
Matches 645; Conservative 0; Mismatches 342; Indels 0; Gaps 0;

Qy      4 ATGTCACAAAGCTTTACATTTGAAACTGCTGACCGTAAACATGATATTAAGCAAGAACATG 63
Db      1 ATGTCACAAAGATACATTTGACATGCTGCGGCGGAGACATTTATTTGGCGAGACGATG 60
Qy      64 GATTTTGCATTTCACTGCGGAGACAGAGTGAATCTCTATCCGCGCGCTTACAGCTGGAAC 123-
Db      61 GATTTTGAATTTGACCTTTACCGGAGAGTGTGCTGTGACATCCGCTGTACAAATGAAA 120
Qy      124 AGTGAAGCTGACGGAAGGCGCCATACAGACAGTACGAGTTATAGGATGCGGAGAAA 183
Db      121 AGTGAAGCGGAGCGGACGAGCATCCCGCGGCTATAGCTTTATCGGATGGGCAAGAG 180
Qy      184 CTGGAATAATATATTTATTTGCGCAGCGCATTAATGAAGCGTTTATCTTTGCGCGCTT 243
Db      181 CTCAGAAATGCTCTGTTTGCAGATGATGTAATGAAGATGCTTTCGCGCGCTT 240
Qy      244 TATTTTCCGCGCTATGCGGAGTACGAAAAACGATACGGGAATACCGTTCACTTGTTC 303
Db      241 TATTTTCCGCGCTATGCTGTGTATGAAAAAGCAAGCAAAAGCCGCAATCTTGC 300
Qy      304 CCGCAATGAGTTTGTGACATGGGTGCTGTCACTGTGCTGCTTTGGAAGCGTAAAGAA 363
Db      301 CCGCAAGAAATTTGTAACATGGGTGCTGTGCAATCGGGAATTTGGAGATGTGAAAAA 360
Qy      364 AAGATTCGATCTTTAACGATTTGAGAAAAAATTAATGATCTATTTGATACAGTTTACCG 423
Db      361 GGGGCTTTCTCTTAAACATTTGAGAGAGAGTCAAGCTTCTGATGATCGGTGACCGCG 420
Qy      424 CTTCATGATATTTGTCAACCGGACGGGCGGAAACCTGACATGAACCAAGAGAGAC 483
Db      421 CTGCATTTGCTATTTAACGACCGCTCCGGGCAAGGTGTGTTTAAACCAAGCGGAC 480
Qy      484 GGGCTCAAGTGTATGATATATCAACCTGTGTATGACAGAACGCCCACTTATATATG 543
Db      481 GGGATTCAAATTCATATATATCCGCTGCGGCTGTGACCAAGATCGGATTTCCCTTG 540
Qy      544 CATGTAAACCAATCTGACGAAATATACAGAAATCAACGGAAGCAATTAAGAGCAAAAG 603
Db      541 CATTTACCAATTTGGCAACTTATCGGCTTCAACCGGACAGTTTGC CGGAAAAA 600
Qy      604 ATGGGCGATTAAGCCCTTCTGCTTTTGGCCAAAGCTTATAGAACTGTGTGCGCGGG 663
Db      601 ATGGGAGGCTGACGCTGTGCTGCTTTTGGTCAAGGTTCCGGGCTGTCCGATTTCCAG 660
Qy      664 GATTATACCGGCTTCCCGGTTTGTCAAGCTGTTTATTTGAAAGCAATCTAGAGCG 723
Db      661 GATTTTACCGGCTTCCCGCTTTGTCAAGGCTGTGATTTTGAAGAGCAATGAAGCT 720
Qy      724 GCGGCGATGAAACGAAAGGTGTACAGCGGCTTTCAATTTTGGCAATATAGAGATA 783
Db      721 GTGTCCGATGAAACAGAAAGCGTCTGCGCGCTTTCAATTTTCCATATGAATAT 780
Qy      784 CCAAGGCGCAGTATGATACGGAAGAGCAAAATTCATATACGAAATATCTGCGTG 843
Db      781 CTTAAGGCGGTGTATGATGATCAAGGGAAGAGCAATTAACCAATATAGCGGATA 840
Qy      844 ATGCAAGCAAACTGGAATCTATTTTCCACCATATGACATCGGCAATTCAAAAA 903
Db      841 ATGTGACGAGACGTCAGCTATTTTCCACCATATTAAGAGAGGAGATTCAAAAG 900
Qy      904 GTAATTTATTTATGAAAGCTTGAAGCTTGTGAGCTTAAAGTGTTCGCTTAAAGCA 963
Db      901 GTTTGCTTATTAAGAGAACTGACAGCAAGAAATTAAGGCGTTTCAAGCAAAAGCAG 960
Qy      964 GAAGAGATTCATGAGCTTAATTA 990

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Db 961 GAAGAGACGGTTCATTCCTCAATCA 987

RESULT 3

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US-10-282-122A-9120
Sequence 9120, Application US/10282122A
Publication No. US20040029122A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EIDTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9120
LENGTH: 984
TYPE: DNA
ORGANISM: Bacillus anthracis
US-10-282-122A-9120
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	Query Match	28.9%;	Score 287.8;	DB 7;	Length 984;
	Best Local Similarity	56.0%;	Pred. 1.2e-75;		
	Matches 544;	Conservative 0;	Mismatches 427;	Indels 0;	Gaps 0;
QY	4	ATGTGCACAAGCTTTACATTGGAAACCTGCTGACCGTAAACATGATATTGACAAGACATG	63		
Db	1	ATGTGACTAGTTTGGACATTAGAGACAAAACCGTCAGCATCTTTTGGACAAGACATG	60		
QY	64	GATTTTGCATTTCAGCTGGGGACAGAGTGATTTCTTATCCGCGCCGTTACAGCTGGAAAC	123		
Db	61	GACTTACATTAGATGATGATACAAAGATAATTAATCATTTCTTCGACATTTCACAGTGGAAT	120		
QY	124	AGTGAAGCTGACGGAAAGGGCCCATCAGACACAGTACGCGTTATTCGATGAGGGGAGAAA	183		
Db	121	AATATTAACGGGTGAATTCATTATTAACGAAACATGCTACGGTCCGAATGGATTAATCAT	180		
QY	184	CTTGGAAATATATTTATTTGCGCAGCGCATTTATGAAACCGGTTTATCTTGGCGCGCTT	243		
Db	181	CAAGGAAGAGATCATTAATAGCGGAGACGAGTAATATAGCAGGATATGACATGTGCACAATTC	240		

OY	244	TATTTTCCGGGCTATGCGGAGTACGAAAAAGATACGGGAAGATCCGTTCAATTGC	303
Db	241	TATTTTCCAGATTGCTACTTATATGCTCAACACATAGATGACACACAAAGAAATTTGGCT	300
OY	304	CCGACATGAGTTGTGACATGGGTGCTGTCAGTCTGTCACTCTTTGGAGAACGTAAAGAA	363
Db	301	CCATTTGATTTTGTAACTTTGGAGTGTGACACAAATTCAATCTGTCAAAAGATTAAAGAA	366
OY	364	AAGATTGCATCTTTACGATTTGTAGAGAAAAAATTAGATCTATTTGGATACAGTTTAACG	423
Db	361	TCTGTAGATGACATTAACCTTTTGGATATACCATTAACCGAATTTAGACCTTACGCCACA	420
OY	424	CTTCACTGATATTGTGACACCGGACGGGCGGAAACCTGACATTTGAACCAAGAGGAC	483
Db	421	CTACATTTGATTTTATAGCGGATTAATGGGAGATTCGACTTTGACTGGATTCGACAGTGA	480
OY	484	GGCCTCAAAGTCTATGATATCAACCTGTGTCAATGACGACGCCGCACTTATATGG	543
Db	481	GGATTTAAATTTGTATGATTAACCACTAGAGATGATGACGAATATGTCCGAGTTTAAATGG	540
OY	544	CATGTAAACAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAGAGACAAAG	603
Db	541	CATTTACAAATTTTAAAGCAATATATAGCCCTTAATGCGACGCCATTGCGCCAAACAG	600
OY	604	ATGGGCGGATATGAGCCCTTTCGCTTTTGGCCAAAGGCTTAGAACTGTGTGTGCGCGGG	663
Db	601	TGGAGTATTTACCACTTATAGTCTTTTGGCCAAAGGCTGAGGCTCAATGGGACTTCCAGGG	660
OY	664	GATTATACACCGCCTTCCCGGTTTGTCAAGACTGTGTTATTTGAAGAACAATAGACCG	723
Db	661	GATTTCAACCCGCAATCGAGGTTTGTGGGGCAGATATGGCAACAAACATTTCAAGT	720
OY	724	GCGGCCGATGAACGAAGGTGTACAGCGCCTTTCAAAATTTGGCAAAATATGACGATA	783
Db	721	ATATATAGCGAAGGAAGGAGATATCAGCCCTTTTCAATCTTATCAAAATTTGTAGGTT	780
OY	784	CCAAAGGCGGAGATACCGGAAGAAAGCAAAATTCATTTATACGCAATATATCTCCGTG	843
Db	781	CTTAAAGGTGAGTATATACGAAGAAAGGTCAATTAATATACATATATACAGCGTA	840
OY	844	ATGTGCAACGAATCTGAAACTACTATTCCACCACTATGACAAATCGGCAATCCAAAA	903
Db	841	ATGTGTATGGAATCCGGAACATATATTTATCACTACTACATTTGTATGACAAATATATAGCT	900
OY	904	GTAATTTTATTTCAAGAAACCTTGACTGTTGTGAAGCCTAAAGTGTTTCCGCTAAAGCA	963
Db	901	GTTCAATTTATTTCAAGAAATTTTATGATACAGATGAGATTAAAGCTATTCGTTCCACGG	960
OY	964	GAGAGAGATAT 974	
Db	961	AAACAAAAAAT 971	

RESULT 4

US-10-282-122A-9817
 Sequence 9817, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangnu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Karl
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ERIIPRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A

Query Match	23.8%	Score 237	DB 7	Length 965
Best Local Similarity	55.5%	Pred. No. 2.5e-60		
Matches 538; Conservative	0	Mismatches 425	Indels 6	Gaps 4

Oy	4	TTGTCACAAGCTTACATATGGAAACTGTCACCGTAACATGATTTAGCAAGAACATG	63
Db	1	ATGTTACTAGTTTGCATTAGACACAAAAACGGTCAGCATCTTTTGCAAGAACGATG	60
Oy	64	GATTTTGCATTTTCAGCTGGGGGACAGAGTGATTTCTTATCCGCGCGTTACAGCTGAAC	123
Db	61	GACCTTCACATTTAGATATGAAATCAGAAAGTAAATATCATCTTCGACATTACAGTGAAT	120
Oy	124	AGTGAAGCTGACGGAAGGGCCCATCAGACACGTAACGGCTTATCGGTATGGGAGAGAAA	183
Db	121	AATATTAACGGCGGAATCATTTAATACGAAACATGTCACGGTCGGAATGGGTATTAATCT	180
Oy	184	CTTGGAAATATATTAATTTGGCAGCGCATTAATGAAAGGGTTATCTGTGCGGGCTT	243
Db	181	CAGGAAGGATCATTAATGCGCGAGTAAATGAAGACAGTTATGACATGTGCACACATC	240
Oy	244	TATTTTCCGGGCTATCCGAGTACGAAAAACGATACGGGAAGATACCGTTCCATTGTC	303
Db	241	TATTTTCCAGGATTCGCTACTTATATGTCAAAGCATATGATGACACACAAAGATTTGGCT	300
Oy	304	CCGACGAGTTTGTGACATGGGTGCTGTGATCTGTCACTTT--GGAAGACGTAAAG	361
Db	301	CCATTTGATTTTGTACTTGGAGTCTGACACAAATTCATCTGTCAAGCGCAGTAAAG	360
Oy	362	AAAAAGTTGCATCTTAAACGATTTGTAGAGAAAAATTAATCATATGATGATAC--AGTTTA	420
Db	361	AATCTGTAGATAGCATTTACCTTTTGGATATACCATTAACCGCATTTAGAGCTTACGCCA	420
Oy	421	CCGCTTCACATGATATTGTACAGCCCGGACGGGCCGAACCTGACGATAGAACCCMAGACA	480
Db	421	CCACTRACATTTGATTTTAGCGGATAAATGGGAGATTTGATTTGTACTGGATCCGACAAGT	480
Oy	481	GACGGCTCAAGTCTATGATTAATCAACTGTGTCTATGACGAACAGCCCGACTTTTA	540
Db	481	GAGGATTTAAATTTGTATGATTAACCACTGGAGTGATGACGATATAGTCGGAGTTTAAT	540
Oy	541	TGGCATGTAAACCAATCTGCAGCAATTAACGAAATCAGACCGGAAGCAATTAGAGACAAA	600
Db	541	TGGCATTTACAAAATTTAAGACAAATATATAGGCGCTTAATATGGAGCCATTTGGCCAAAC	600

Oy	601	GAGATGGGGGGAATTGACCCCTTTCTGCTTTGGCCAGGCTTAGGAACTGTGGCTGCCG	660
Db	601	GAGTGGAGTAATTACATTAAATGCTTTTGGCCAGGCTCGGCTCAATGGACCTTCCA	660
Oy	661	GGGGATTATACACCGCCTTCCTCCGGTTGTGCAGACTGTATATTTGAAAGAACACTAGAG	720
Db	661	GGGGATTATACCCCGCCCATCGAGGTTGTGGGGCAGACATATGGCAAAACAACTCA	720
Oy	721	CCGGCGGCCGATGAACAAGAGGTGTAAACAGCCGCTTTCAAAATTTGGCAAAATAGACG	780
Db	721	GGTATGATAGACGAAGAAAGAGGAGTATCACCCCTTTTCAATCTTATCAAAATGTGAG	780
Oy	781	ATACCAAGAGGGCGCAGTGAATAACGGANAAAGCAAAATCAATTATAGCAATATA--CTTC	839
Db	781	GTTCCTAAAGGTGGAGTAAATTAACAGAACAGGTGCATTAGATTAATACCARATATACCAAG	840
Oy	840	CGTGAATGCAACGAACCTGAAACTACTATTTCCACCACTATGACAAATCGG--CAAAATC	897
Db	841	CGTAATGTGGAGTAATCCGGAACATATTATTATCTTACTTAACAAATGTAGACCAATTA	900
Oy	898	CAAAAAGTAAATTTATTTATGANAAGACTTGACGTTTGGAGCCTAATAGTGTTCGGCT	957
Db	901	TACCTTGTCATTTATTTCTCGAAAAATTAGATACCGATGGAATPAAAGCTATCCCTTC	960
Oy	958	AAAGCAGAA	966
Db	961	CAACCGAA	969

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Query Match	23.4%	Score 232.6;	DB 7;	Length 990;
Best Local Similarity	53.0%	Pred. NO. 5.5e-59;		
Matches 496;	Conservative 0;	Mismatches 439;	Indels 0;	Gaps 0;

QY 4 ATGTGCACAAAGCTTCAACATTGGAAACCTGTGACCGGAAACAGATATTAGCAACAAATG 63
Db 1 ATGTGCACAAAGCTTGTATTTAGAAACGTTAGATGGAAACATTTATTATTCAGAAACGATG 60
QY 64 GATTTTGCATTTCAAGCTGGGGACAGAGGTGATTTCTTATCCGGGCCGTTACAGCTGGAAC 123
Db 61 GATTTTGCATTTTATTTTGGAGGCAACCAACAATTAGCCCAAGAAATATTGATGGAAA 120
QY 124 AGTGAAGCTGACGGAAAGGCCCATACAGACACAGTACGCTTTATCCGTATGGGGAGAAA 183
Db 121 TCTTCTACAGACGGGCGCCATTTATTTAATAGATAGCATTTGTTGGACGGGAAAGGAG 180
QY 184 CTTGGAATAATTTAATTTTGGCAGCCGATTAATGAAGGGTTATCTTGTGGCGCCTT 243
Db 181 TTAGATTAATTAACATTTTCCAGACGGATGTAATGAAGGATTAAGCTGTGATCTCTA 240

OY 244 TATTTTCCGGGCTATCGGAGTACGAAAAACAATACGGGAAGTACCGTTCATTGTC 303
 Db 241 TATCTTCCAGGAGAACCAAGTTTATCGGCCACACCACTGAGAGAAAAATCAATTTAGCT 300
 OY 304 CCGCATGAGTTGTGTGACATGGGTGTGTCACTGTCTCAAGTCTTTGGAGAAGCGTAAAGAA 363
 Db 301 CCACAGAATTTTGTGGCTTGGCTGTAGGAACCTGGCGAACGATTTAAAGATGTGAAGCA 360
 OY 364 AAGATTGCATCTTACGATGTGTAGAGAAAAAATTTGATCTATTTGATACAGTTTAAACG 423
 Db 361 AAGTTATCGGTTATTAACCTTGGTGATTCACCAAGTACCGTTACTTGGAAATCACACCA 420
 OY 424 CTTCCTGATATTTGTCAAGCCGAGCGGCCGAAACCTGACGATAGAACCCAGAGCAGAC 483
 Db 421 TTACACTGGATTTTCAACAGCAAGAGTGGCGCTGTGTAGTGAATGAAACCAACAGAAAC 480
 OY 484 GGGCTCAAAAGTCTATGATATCAACCTGTGTATATGACAAAGCCCCGACTTATATGG 543
 Db 481 TCGCTTCGTATTAAGAAAAAACCCTGTAGAGATTATACAATCGCACGATCGAATGG 540
 OY 544 CATGTAAACCAATCTGCAGCAATATACAGCAATCAGACCGAGCAATTTAGAGCAAAAGAG 603
 Db 541 CATATCGAAGATTTACGAACATACAGAGTTTACAGCAACAAATTTAGCCGGGTGAAG 600
 OY 604 ATGGGCGATTAGCCCTTTCTGTCTTTGGCCAAAGCTTAGAACTGTGGTCTGCCGGGG 663
 Db 601 TTCGAGAGTATATGGCTTAACCATTTTGGCAAGGTACAGGAACAAGCAATTAACAGGT 660
 OY 664 GATTATPACCGGCTTTCCCGGTTTGTGCAGAGCGTTTATTTGAAAGAACCTAGAGCCG 723
 Db 661 GGTATATCTCCGCCAGAACGTTTGTTCGTGCGGCAATCTTGAAAGAAAATATTTAATA 720
 OY 724 GCGGCGCATGAACAGAAAGGTGTAAACGCCGCTTTCAATTTTGGCAATATGACGATA 783
 Db 721 GCGAAAAACGAAGAAAGCACTATCACAATGTGTGTATGTCTTGAACAGTGCAGCAT 780
 OY 784 CCAAGGGGCGCGATTAACGAAAGAACGAAATCATATACGAATTAATCTCCGAG 843
 Db 781 CCGAATGGAGCGGTATTTAAAGAAAGGTGTGACCTGATTTCAACAATATGTGGCATCT 840
 OY 844 ATGTGCAACGAAACTGAAACTACTATTTTCCACCACTATGACAAATCGGCAAAATCCAAAA 903
 Db 841 ATGTGTTGCGAAAGCAAAACGTACTATTTCACTCTATACGAAACAAACAAATCAATAGT 900
 OY 904 GTAATTTATTTCAAGAAAGCCTTACCTGTGGGA 938
 Db 901 GTTACTTGTGCAAGAAAGTTATAGAAATATAGAA 935

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RESULT 6
US-10-398-221-2682
Sequence 2682, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, gen
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398, 221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 06
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2682
LENGTH: 990
TYPE: DNA
ORGANISM: Listeria monocytogenes EGD
US-10-398-221-2682

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Query Match 23.4%; Score 232.6; DB 7; Length 990;

Best Local Similarity 53.0%; Pred. NO. 5.5e-59;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

OY	4	ATGTGCAAAAGCTTACATATGGAAAATCGTGACCGTAAACATGTAATTAGCAAGAAATG	63
Db	1	ATGTGCAAAAGCTTGTATTAAGAAAGTTAAGATGAGAAAACATTTATTAACAGAACATG	60
OY	64	GAATTTGCATTTCAAGTGGGGAACAAGTGATTTCTATCCGCGCGTTACAGCTGGAC	122
Db	61	GAATTTGCTTTATTTTGAAGCGAACCCAAACATTAGCCAAAGAAATTAATGATGAAA	120
OY	124	AGTGAAGCTGACGGAAGGGCCCATCAGACACAGTACCGCTTATCGGTATGGGAGAAA	183
Db	121	TCCTTACAGAGGGGCGCAATTAATTAAGATAAGCATTTGTTGGAAGCGGAAAGAG	180
OY	184	CTTGGAAATATATTTATTTGCGACGGCATTAATGAAGGGGTTATCTTGCGCGCTT	243
Db	181	TTAGTAAATATACATTTTGGCAGACGGATGAATGAAGAAATTAAGCTGTGCATCTTA	240
OY	244	TATTTTCCGGGCTATGCGGAGTACAGAAAACGATACGGGAAGATACCGTTCCATTTGC	303
Db	241	TATCTTCCAGGAGAGCAATTATGCGCAGCACAGTGGAGAAAATCAATTTAGCT	300
OY	304	CCGCATGAGTTGTGACATGGGTGCTGATCTGTCAATCTTTGGAAAGCTTAAAGAA	363
Db	301	CCACAGAAATTTTCTTTGGCTGTAGGAACTTGGCACAAGTATAAAGATGGAAGCA	360
OY	364	AAGATTCATCTTTCACATTTGTACAGAAAAATTAAGATCTATTTGGATACAGTTTACG	423
Db	361	AAGTTATCGGTATTAACCTTGTGTGATCAACGATCCGTACTTGGAAATCACACCCA	420
OY	424	CTTCACTGGAATATTTGTACAGCCGACGGCCGAAACTGCACATAGAACCAAGACAGAC	483
Db	421	TTACACTGATTTTACAGACAAAGATGGGCGTTGTGTAGTGAATTAACCAAGAAACA	480
OY	484	GCGCTCAAAAGTCTATGATTAATCAACCTGGTGTCTATGACGAACAAGCCCGACCTTATATGG	543
Db	481	TGCGTTCGTATAAAGAAACCCTGTAGGAGTTATGACAAATACGCCACGATCGAATGG	540
OY	544	CATGTAAACCAATCTGCAGCAATATACAGGAATCACAGCGAAGCAATTAGAGACAAAG	603
Db	541	CATATCGAAATTTACGACATACACAGGTTTACAGCAACACATTAAGCCGCGTGAAG	600
OY	604	ATGGCGGATTAAGCCCTTTCTGCTTTTGGCCAAAGCTTAGAATCTGTGGTGGCCGGG	663
Db	601	TTCCGAGAGTATATGCGTAAACCATTTTCCGAAGTACAGAAACAAGCAATTAACAGGT	660
OY	664	GATTATACACGGCTTTCCCGTTTGTCAAGCTGTTATTTGAAGAACAATCTAGAGCG	723
Db	661	GATTATACCTCCGCCAGACGTTTGTCCGTGCGGCATTACTTGAAGAAATATTTAATAA	720
OY	724	GCGGCGGATGAACGAAAGGTGTAACAACCGCTTTTCAAAATTTGGCAATATGACGATA	783
Db	721	GCGAAAAACGAAAGAGCTATCAAAATGTGTGTATGTTGAACAGTCCGCAAT	780
OY	784	CCAAAGGCGCAGTGATTAACGAGAGAAACGAAATTCATTAACCAATATATCTTCGTG	843
Db	781	CCGATAGGAGGGTATTAAGAAAGTGTGACCTGATTTCAACAATATGTGGCATCT	840
OY	844	ATGTGCAACGAACCTGGAACCTACTATTTCCACCACTATGACATGCGCAATCCAAAA	903
Db	841	ATGTGTTCCGAAAGCAAAACGTACTATTTCACTCATTCGAAAAACAACCAATCATAGT	900
OY	904	GTAATTTATTTCAATGAAGACCTTGACGTTTGA	938
Db	901	GTAATTTGTGAAAGAAAGTATTAAGAAATATGA	935

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RESULT 7
US-10-282-122A-24755
; Sequence 24755, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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APPLICANT: Wang, Liangau
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyleh, K.
APPLICANT: Xu, H.
FILE REFERENCE: Identificaiton of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 24755
LENGTH: 990
TYPE: DNA
ORGANISM: Listeria monocytogenes
US-10-282-122A-24755

Query Match      23.4%; Score 232.6; DB 7; Length 990;
Best Local Similarity 53.0%; Pred. No. 5.5e-59;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

OY 4 ATGTGCAAGCTTACATTGGAAGAACTGACCGTAAACATGATTAGCAAGAACATG 63
    |||||
DB 1 ATGTGCAAGCTTACATTGGAAGAACTGACCGTAAACATGATTAGCAAGAACATG 60
    |||||

OY 64 GATTTTCATTTGACCTGGGAGACAGAGTATCTTATCCGCCGCTTACAGCTGAC 123
    |||||
DB 61 GATTTTCATTTGACCTGGGAGACAGAGTATCTTATCCGCCGCTTACAGCTGAC 120
    |||||

OY 124 AGTGAAGCTGACGGAAGGCGCCATCAGACACAGTACCGCTTATCCGTAAGGAGAAA 183
    |||||
DB 121 TCTTTCACAGACGGTGCATATATATATATATATATATATATATATATATATAT 180
    |||||

OY 184 CTGGAAGATATATATATATATATATATATATATATATATATATATATATATATAT 243
    |||||
DB 181 TTGATATATATATATATATATATATATATATATATATATATATATATATATAT 240
    |||||

OY 244 TATTTTCGGGCTATGCGAGTACGAAAAAAGATACGGAAGATACCTTCATTTGTC 303
    |||||
DB 241 TATCTTCAGAGAGAGAGGATTTATGCGCCAGCAGCAAGTGAAGAAAAATCAATTTAGCT 300
    |||||

OY 304 CCGAGTAGTTTGACATGGGTCGTCTGTCTGTCACTTTTGAAGAGCTTAAAGAA 363
    |||||
DB 301 CCACAGAAATTTTGTCTTGGCTTTAGGAATTTGCCAGAGATTAAGATGTGAAGCA 360
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OY 364 AAGATTCGATCTTTAAGATTTGAGAAAAAATAGATCTATTTGATACATTTTACCG 423
    |||||
DB 361 AAGTATCGGTTATATTAATTTGGTGTATCAACAGATACCGTTACTTGAATATCA 420
    |||||

OY 424 CTTCATGATATTTGTCAGACCGGACCGGCGAAACCTGACGATGAACAGAGACAG 483
    |||||
DB 421 TTACACTGATTTTCAACAGACAGAGTGGCGCTGTGTATGATATTAAGCAACAGAA 480
    |||||

OY 484 GGCCTCAAGTCTATGATATATCAACCTGTGTATGATGACAGACGCGCCGACTTATATG 543
    |||||
DB 481 TCGCTTCGATATTAAGAAAAACCTGTAGAGATTAAGCAAAATACGACAGCATGATG 540
    |||||

OY 544 CATGTAAACCATCTGACAGATATTAAGAAATCAAGCCAGCAATTTAGAGACAAAG 603
    |||||
DB 541 CATATGAGAAATTTACGCAATACAGGTTTAAAGCAACAAATATACGCGCGTGAAG 600
    |||||

OY 604 ATGGCGGATTAAGCCCTTTGCTTTGGCCAGGCTTAAAGAACTGTGGTCCGCGGG 663
    |||||
DB 601 TTGAGAGATATATGCTTAAACCATTTTGGAGTACAGAAACAAATTTACAGGT 660
    |||||

OY 664 GATATATACACGCTTCCGCTTTGTCAGAGCTGTTTATTTGAAGAACATCTAGACCG 723
    |||||
DB 661 GGTATATCTCCGCGCAGAACGTTTGTCCGTGGCATCTTGAAGAAATATTAATAA 720
    |||||

OY 724 GCGGCGGATGAACAGAAAGTGTAAACGCGCTTTTCAATTTTGGCAATATAGAGAT 783
    |||||
DB 721 GCGAAAGAAAGAAAGAAAGCTATCAAAATGTGTGTATGCTTGAACAGTGTCCGAT 780
    |||||

OY 784 CCAAGGCGGCGAGTATTAAGAGAAAGCAAAATCATTTATACGATATATCTCCGT 843
    |||||
DB 781 CCGAATGAGCGGTATTAAGAAAGTGTATGACCTGATTTTACACAAATATGTGCATCT 840
    |||||

OY 844 ATGTGCAAGAACTGGAATCTATATTTTCAACCATATGACATGCGAAATCCAAAA 903
    |||||
DB 841 ATGTGTCGGAAGAAAGAAAGCTATTTTCACTGATATGAAACAAACAAATCAATAGT 900
    |||||

OY 904 GTTAATTTATTTCAATGAAGAACCTTGAAGCTTTTGA 938
    |||||
DB 901 GTTACTTGTTCGAAGGAAGTATTAAGAAATATGA 935
    |||||

RESULT 8
US-10-429-802-17
Sequence 17, Application US/10429802
Publication No. US20030228285A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: WONG, KA YIN
APPLICANT: ZOU, YIYU
FILE REFERENCE: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
FILE REFERENCE: UTSC.752US
CURRENT APPLICATION NUMBER: US/10/429,802
PRIOR FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 17
LENGTH: 1616
TYPE: DNA
ORGANISM: Bacillus sphaericus
US-10-429-802-17

Query Match      17.4%; Score 173.8; DB 6; Length 1616;
Best Local Similarity 49.8%; Pred. No. 4.1e-41;
Matches 495; Conservative 0; Mismatches 492; Indels 6; Gaps 2;

OY 7 TGACAGTCTTATCATTTGAAACTGACCGTAAACATGATTTAGCAAGAACATGAT 66
    |||||
DB 335 TGACAGTCTTATCATTTGATCAATTTGTCACAGATGATTAAGTTATTCGCTCCACAAATGAT 394
    |||||

OY 67 TTGCACTTCACTGGGAGACAGAGTGTCTATCCGCGCGGTTACAGCTGAACAGT 126
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Db 395 TTACAGTGAACACAGATAGTAAAGTATTATGTCACGTAATTACGCAATTCGATTG 454
Qy 127 GAAGCTGACGAA---GGGCCATCAGACACAGTACGCGTTATTCGTAATGGGAGAA-- 181
Db 455 TTAGAAAAAGAAATAGTACATTAACAATTCAATGCTTTTGTGTAATGGGAGACACT 514
Qy 182 -AACTGGAAATATATATTTGCGGACGCGCATTAATGAAGCGCTTATCTGTGGGGG 240
Db 515 GACATTAATCAACCGCTTCTATATGATGGGTAACGAAAGAGGATTAATGGCGCGAATG 574
Qy 241 CTTTATTTTCCGGGCTATCGGAGTACGAAACGATACGGGAGATACCGTTCACTT 300
Db 575 CTTTACTATGTAACATTTGCGACTATGCTGACGAACCTTAAAGGCAACAGGCAATC 634
Qy 301 GTCCCGCATGAGTTGTGACATGGGCTGTGATCTGTGCACTTTTGGAGAAGCTTAA 360
Db 635 AATCCGCTGATGATTTCTCAAGTTTGAAGAAATGTGTAACTGTCATGATGTAT 694
Qy 361 GAAAGATTCGATCTTTACGATGTAAGAAATTTAGATCTATTTGATACGTTT 420
Db 635 GAAATTTACTTCTTATATATTTAATTAAGAGGCAATATATATCTTGGCTTTCACCC 754
Qy 421 CCGCTTCACTGATATTTGACAGCGGACGCGCAACCTGACGATAGAACCAAGAGA 480
Db 755 CCACTTCACTATACATTTACAGATGCTTGTGTAATGATTTGTAATGACCGGATTA 814
Qy 481 GAGCGCTCAAAAGCTATGATATCAACCTGTGTATGACGAGACGCGCCGACCTTTA 540
Db 815 ACAGGCATTAACCATTCATCGAAGAAAGATTTGCGTCATGACGATATGCGCTGATGA 874
Qy 541 TGGCATGTAACCAATCTGACAGCAATATACAGAAATCAAGCAAGCAATTAAGAGCAA 600
Db 875 TGGCATGACAGCAATTTAAGCTTACATTTGTGTACACCAATCCGCAACAGATTA 934
Qy 601 GAGATGGGCGGATTAACCTTCTGCTTTTGGCCAAAGGCTTGAAGTGTGTCGCG 660
Db 935 ATGATGGGAGACTTGTGATTTGACACCGTTTGGGCAAGGCGGCGCTTGAATTAACA 994
Qy 661 GGGGATTAACACGCGCTTCCGCTTGTGTGACAGCTGTTTATTTGAAAGAACATCTAG 720
Db 995 GGTGATTTACGCGCTGACAGCGTTTCTTGGGAGACACTGAAATTAATATCTGA 1054
Qy 721 CCGGCGCGCGGATGAACGAAAGGTGTACAGCGCTTTTCAATTTTGGCAATATGACG 780
Db 1055 AAAGCAGAAATGAAGAGGAGGCTTAACTTGTTCATTTCTTCTCTGTAAAT 1114
Qy 781 ATACCAAGGCGCGAGTATACGAGAAAGCAATTCATTTATACCAATATATCTTCC 840
Db 1115 ATCCCAAGAGGCTTGTGTTTGAACAATGAGGAGAAACGATTAATCACTATACCTCA 1174
Qy 841 GTGATGTGCAAGAACTGGAATCTATTTTCCACCACTATGACAAATCGGCAATCCAA 900
Db 1175 GCTATGTGTGCAAAAGTAAATTAATTAATTAATGATGACAAATGACAAATTTCA 1234
Qy 901 AAAGTAAATTTATTTCAAGAGACCTTACCTTTGAGCCTTAAAGTGTTTCCGCTAA 960
Db 1235 GCGCTTCTTAAAGGCTGAAATTTAATTAATGCTAAAGTTTAACTATTTGAGTGGAT 1294
Qy 961 GCAGAGAGGATTTCAATGAGCTTAATTAAGGA 993
Db 1295 CGTAAACAGATTTAAGCAATTAATCAAGTA 1327

RESULT 9

US-10-430-503-8
; Sequence 8, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAM-CHING
; APPLICANT: LAN, KENG-HSIN

; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
; FILE REFERENCE: REAGENTS
; FILE REFERENCE: UTSC:79705
; CURRENT APPLICATION NUMBER: US/10/430,503
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/383,063
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1616
; TYPE: DNA
; ORGANISM: Bacillus sphaericus
US-10-430-503-8
Query Match 17.4%; Score 173.8; DB 6; Length 1616;
Best Local Similarity 49.8%; Pred. No. 4,1e-41;
Matches 495; Conservative 0; Mismatches 492; Indels 6; Gaps 2;
Qy 7 TGCACAGCTCTTACATTTGGAATCTGTCACCGTAAACATGTAATGACAAAGCAATGAT 66
Db 335 TGCAGTACCTTATCAATTCGTACAAAGATGTAATTAATGCTGCGACAAATGAT 394
Qy 67 TTTGATTTCACTGCGGACAGAGGTATCTTATCCGCGCGCTTACGCTGGAACAT 126
Db 395 TTACAAATGAACAGATGTAAGTATTTGTCACGTAATTAACGCAATTCGATG 454
Qy 127 GAAGCTGACGAA---GGGCCATCAGACACAGTACGCGTTATTCGTAATGGGAGAA-- 181
Db 455 TTAGAAAAAGAAATAGTACATTAACAATTCAATGCTTTTGTGTAATGGGAGACACT 514
Qy 182 -AACTGGAAATATATATTTGCGGACGCGCATTAATGAAGCGCTTATCTGTGGGGG 240
Db 515 GACATTAATCAACCGCTTCTATATGATGGGTAACGAAAGAGGATTAATGGGAGACACT 574
Qy 241 CTTTATTTTCCGGGCTATCGGAGTACGAAACGATACGGGAGATACCGTTCACTT 300
Db 575 CTTTACTATGTAACATTTGCGACTATGCTGACGAACCTTAAAGGCAACAGGCAATC 634
Qy 301 GTCCCGCATGAGTTGTGACATGGGCTGTGATCTGTGCACTTTTGGAGAAGCTTAA 360
Db 635 AATCCGCTGATGATTTCTCAAGTTTGAAGAAATGTGTAACTGTCATGATGTAT 694
Qy 361 GAAAGATTCGATCTTTACGATGTAAGAAATTTAGATCTATTTGATACGTTT 420
Db 635 GAAATTTACTTCTTATATATTTAATTAAGAGGCAATATATATCTTGGCTTTCACCC 754
Qy 421 CCGCTTCACTGATATTTGACAGCGGACGCGCAACCTGACGATAGAACCAAGAGA 480
Db 755 CCACTTCACTATACATTTACAGATGCTTGTGTAAATGCAATGTTATGAACCGGATTA 814
Qy 481 GAGCGCTCAAAAGCTATGATATCAACCTGTGTGACGAGACGCGCGCATTTATA 540
Db 815 ACAGGCATTAACCATTCATCGAAGAAAGATTTGCGTCATGACGATATGCGCTGATGA 874
Qy 541 TGGCATGTAACCAATCTGACAGCAATATACAGAAATCAAGCAAGCAATTAAGAGCAA 600
Db 875 TGGCATGACAGCAATTTAAGCTTACATTTGTGTACACCAATCCGCAACAGATTA 934
Qy 601 GAGATGGGCGGATTAACCTTCTGCTTTTGGCCAAAGCTTGAAGACTGTTGTGCGG 660
Db 935 ATGATGGGAGACTTGTGACACCGTTTGGGCAAGGCGGCGCTTATGAGATTAACA 994
Qy 661 GGGGATTAACACGCGCTTCCGCTTGTGACAGCTGTTTATTTGAAGAAACATCTGAG 720
Db 995 GGTGATTTACGCGCTGACAGCGTTTCTTGGGAGACACTGGAAGAAATTAATCTGA 1054
Qy 721 CCGGCGCGCGGATGAACGAAAGGTGTACAGCGCTTTTCAATTTTGGCAATATGACG 780
Db 1055 AAAGCAGAAATGAAGAGGAGGCTTAACTTGTTCATTTCTTCTGTAAAT 1114
Qy 781 ATACCAAGGCGCGAGTATACGAGAAAGCAATTCATTTATACCAATATATCTTCC 840

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Db      1115 ATCCAAAGAGTGTGTTTGAACAATGAGGGGAAAAAGGATTAATACATCTATACCTGA 1174
OY      841 GTGATGTCGCAAGAACTGGAACATCACTATTTCACGACTGTGCAATGGCAAAATCCAA 900
Db      1175 GCTATGTTGTCACAAAGTAAACATTAATCTTTAACTGTATGCAAAATAGTGAATTTCA 1234
OY      901 AAAGTAATTTATTTTCATGTAAGACCTTACTGTTTGGAGCCGTAAAGTGTTCGCTAAA 960
Db      1235 GCCGTTTCCTTAATGCGTGAATAATTAATAGTCAAGATTAATTAATCACTTTGAGTGGAT 1294
OY      961 GCAGAGAGAGTATTCACTAGACTTAATTAAGA 993
Db      1295 CGTAAACAAGATATTAAACAATTAATCAAGTA 1327

RESULT 10
US-10-282-122A-34300
; Sequence 34300, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34300
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34300

Query Match      16.1%; Score 160.2; DB 7; Length 978;
Beet Local Similarity 49.9%; Pred. No. 4e-37;
Matches 458; Conservative 0; Mismatches 453; Indels 6; Gaps 2;

OY      4 ATGTGCACAAGCTTACATGGAACCTGCTAGCCGTAAACATGTTTGGCAAGAACATG 63
Db      1 ATGTGTACGGCTAATTTCTTATATACAAAACAAGCTTATCATATTATTGCTGAACGATG 60

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QY	64	GATTTGGATTTCACTGGGGGACAGAGGGAATTCCTCAATCCGGCCGTTACACATGGAAAC	123
Db	61	GACTTTGCATTTGAATTTAATGATATCCCAACCAATTTGTTCCAGCTATTATCACTACCA	120
QY	124	AGTGAAGTGCACGGAGGGCCCATCAGACACAGTACGCGTTATCCGTATGGGAGAAA	183
Db	121	TTTGATCTTAGATTC---GACATGCGCTTGGAAATGTTTTGTTGGAACCAATTTAAAA	177
QY	184	CTTGAATTAATATATTTTGGCCGACGTCATTAATGAAGGGTTTATCTTGGCGGCTT	243
Db	178	GTAGACCTTATAGTTTGTGATGATGATTAACGAAAAAGTTTACTATTTGAAACCAT	237
QY	244	TATTTTCCGGGCTATGCGAGTACGAAAAACGATACGGAAAGATACCGTTCAATTTGC	303
Db	228	TACTTCACTGGGAGCGCTCATACAGTACCCATTAACGTTATGTTATTTAACTTAGCA	297
QY	304	CCGATGATGTTTGTACATGGGTGCTGTCAAGTCTGACCTTTTGGAAAGCGTAAAAAA	363
Db	298	CTTGAGGATTTATGTTGGGTTTAAAGTTTAAATGAATTAAGCGAATTTAAACAA	357
QY	364	AAGATTCATCTTTACGATTTGAGAGAAAAAATTAAGATCTATTTGATACAGTTTACCG	423
Db	358	AAAGTTAAGAAGATCAATATTAATGAATGAATAAATAACAATTTGAATTCGTTCCCT	417
QY	424	CTTCACTGGATTTGTCAAGCCGACGGGCGGAACCTGACATTAAGATCAACAGACAG	483
Db	418	TTACATTTTCATGCTCATGATGAAAACAGACATACCGTACCAATACCTCAAAATGGC	477
QY	484	GGCCCAAGTCTATGATATCAACCTGGTGCATGACGAACAGCCCGACTTATATATG	543
Db	478	TTATTAATAGTTAAAGATTAATTTGTTCACTACTTACAAATGCGCTTAATTAATGATGG	537
QY	544	CATGTAAACAATCTGACGCAATATACAGGAATCAAGCCAGACATTTAGAGCAAAAG	603
Db	538	CATCATATCTAATCTTAAGAAATTAATGCTTATTTTAAACCAAGAAATCAACCAATCAATTA	597
QY	604	ATGGCGGATTAAGCCCTTTGCTTTGGCCAAAGCTTATGAACTGTGGTGCACCGGG	663
Db	598	ATAGTTAAAGTCTCTAGTAAGATCAATGGGTTGTGAAGCAGGAACAATGGCTTACCGGGT	657
QY	664	GATTTAACACCGGCTTCCCGGTTTGTCAAGGCTGTTTATTTGAAAGAACATCTAGAGCCG	723
Db	658	GGTTATACCTTCAACGAAGCGTTTATTAACGGGCTACATTTTAAGACCACTACGCTGT	717
QY	724	GCGGCGCATGAACGAAAGGTGTACAGCCGCTTTCAATTTTGGCAAAATAGACATA	783
Db	718	TCCCATTAATGAAGATGAATAATTTAATGAAATTTTAAAGTTCTAAGATCAGTCAATC	777
QY	784	CCAAAGGGGCGAGTATTAACGAAAGACGAAATTCATTAATCGCAATTTACTTCCGTG	843
Db	778	CCTCAGAGTGCGATTT---CGATGCCAATTAATTAATCACTTACACAGATATCAATTAGTG	834
QY	844	ATGTGCAAGAACTGGAATCTATTTTCCACCACTATGACAAATCGGCAATCCAAA	903
Db	835	ATGGAAGTAAAGAAAGAAAGCTATTAATTAATTAAGCCTACTTATAGTATCAAAATTTTCAA	894
QY	904	GTAATTAATTTCAATGA	920
Db	895	ATTAATTAATTTCAATGA	911
RESULT 11			
US-10-724-972A-1455			
Sequence 1455, Application US/10724972A			
Publication No. US20040147734A1			
GENERAL INFORMATION:			
APPLICANT: Doucette-Stamm, Lynn			
APPLICANT: Bush, David			
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS			
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS			
FILE REFERENCE: PAT03-16			
CURRENT APPLICATION NUMBER: US/10/724,972A			
CURRENT FILING DATE: 2003-12-01			

PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO: 1455
LENGTH: 996
TYPE: DNA
ORGANISM: S. epidermidis
US-10-724-972A-1455

Query Match 16.0%; Score 159; DB 7; Length 996;
Best Local Similarity 49.8%; Pred. No. 9, 2e-37;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTGCAAGCTTACATTGGAAGTCTGACCGTAAACATGATTAGCAAGACA 61
DB 14 ATATGTGCAAGCTTACATTGGAAGTCTGACCGTAAACATGATTAGCAAGACA 73
QY 62 TGGATTTGCAATTGAGCTGGGAGACAGAGTATCTCTATCCGCGCGTTACAGCTGA 121
DB 74 TGGACTTGCATTGAATTTAATGATCCCAACATGTTCCACGCAATTAATCACTAC 133
QY 122 ACAGTGAAGCTGACGGAAGGCGCCATCAGACAGTACCGTTATTCGGTATGGGAGAA 181
DB 134 AATTGATCTAGATTCAAGCATGCTCTT--GAATATGTTTGTGGACAAATTTAA 190
QY 182 AACTGGAATATATATTTTGGCGACGCGATTATGAAGCGGTTATCTGTGCGCGC 241
DB 191 AAGTAGGACGTTATGATTTGGTATGATTAAGAAAGGTTAGCTATTTGAAAC 250
QY 242 TTTATTTTCCGGGCTATCGGAGTACGAAAAACATACGGAATACCTGTCATG 301
DB 251 ATATCTTACGTTAGAGCTTCAATACGATCCATTAACGTTATGTTTAACTTAA 310
QY 302 TCCCGCATGATTTGTGACATGGGTGCTGTCACTGCTTGTGGAAGACGTAAG 361
DB 311 CACCTGAGAGTTTATTTGTTGGTTTAAAGTTTAAAGTATTTAGCAATTTAAAC 370
QY 362 AAAAGATTCGATCTTTAAAGATTTAGAAAAAATTAGATCTATTTGATACAGTTTAC 421
DB 371 AAAAGTTAAGAAATCAATATTTAGATGAAGAAAAATACGACTTTGAATTCGTTCTC 430
QY 422 CGCTTCACTGATATTTGACAGCCGAGCGGCGAAACCTGACATTAACCAAGACAG 481
DB 431 CTTTACATTTCTATGCTCATATGAAACAGACATACCGTACCTTAACCTCAATG 490
QY 482 ACGGCTCAAGTCTATGATATCACTGTTGTCATGACGAAAGCGCCGATTTATAT 541
DB 491 GCTTATTAATGTTAAGATTAATTTATGTTTACCTTAACAAATGAACTTAATTAAT 550
QY 542 GGCATGTACCAATCTGACAGCAATTAACAGAAATCAGCCAGCAATTTAGAGCAAG 601
DB 551 GGCATGTATCACTTAAGAAATTAACGCTTTTAAAGCCACAGAAATCAACATCAT 610
QY 602 AGATGGGCGATTAAGCCCTTTCTGCTTTGGCCAAAGGTTAGAACTTTGCTGCGG 661
DB 611 TAAATGTTAAGTCTAGTAAGATCAATGGGCTGTGAAGCAAGAAATGCTTAAACG 670
QY 662 GGGATTTAACAAGCCCTTCCGTTTGTGACAGCTGTTTATTTGAAAGCAATCTAGAGC 721
DB 671 GTGTTATAGTCAACAGATGTTTATAGCGCTTACATATTTAAGACCAATCAAGCT 730
QY 722 CGGCGCGCATGAACGAAAGGTCTAACAGCGCTTTTCAATTTTGGCAATATGACGA 781
DB 731 GTTCCCATTAATGAAGATGAATTAATGAATTTGTTTAAAGTCTTAAGATCACTGTA 790
QY 782 TACCAAGGCGCGATTAACGAGAGAAATTCATTATAGCAATATATCTTCCG 841

DB 791 TCCCTCAAGTGCATTTAT---CGATGCCAATTAATACATTACACAAATATCAATTAG 847
QY 842 TGAATGCAAGCAAGTGAAGTCTATTTTCCACCATATACATGCGGAAATCCAA 901
DB 848 TGAATGCAAGTGAAGTGAAGTCTATTTATTTAACCTTACTTATGCAATCAAAATTTCA 907
QY 902 AAGTAAATTTATTTTCATGA 920
DB 908 AATTAATTTAATCAAGCA 926

RESULT 12

US-10-282-122A-7960
Sequence 7960, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EILTRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PAM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 7960

LENGTH: 993

TYPE: DNA

ORGANISM: Staphylococcus aureus

US-10-282-122A-7960

Query Match 14.7%; Score 146; DB 7; Length 993;
Best Local Similarity 47.5%; Pred. No. 7, 7e-33;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

QY 4 ATGTGCAAGCTTACATTGGAAGTCTGACCGTAAACATGATTAGCAAGACAATG 63
DB 1 ATGTGCAAGCTTACATTGGAAGTCTGACCGTAAACATGATTAGCAAGACAATG 60
QY 64 GATTTGCAATTGAGCTGGGAGACAGAGTATCTCTATCCGCGCGCTTACAGTGAAC 123
DB 61 GATTAATGATTAATCAATGATGTTGCGCAGCAGTACGCTTGAATTAATTCGTTGACA 120

124 AGTGAAGCTGACGGAAGGGCCATGACACAGTACCGCTTATCGGTATGGGAGAAA 183
 121 TCTCCACT--GGACGACAGAGCCAAAGCAATATGCTTTATTTGTCAGAGAACAT 177
 184 CTGGAATAATATATATTTGCGGACGATTAAGAAAGCGTTTATCTGTGCGGCTT 243
 178 ATGGAAGGTTTATTTATGATGATGATGATTAAGAACATGGGCTTCTATTTGACACA 237
 244 TATTTTCCGGCTATGCGGAGTACGAAAAACGATACGGGAAGTACCTTCACTTGC 303
 238 TATTTCCGAGTTATGTTATATATGCTCAACACAAAGCGGACCGGATGATATTAG 297
 304 CCGAGATGATTTGTCATGGGCTGTCAGTCTGCACTCTTTGGAACGTAAGAAA 363
 298 CAAATGAAATGTCATGATGATTTGGATATACAAAGCATTTAGATATGAAACAA 357
 364 AAGATTCGATCTTTAAGATTTAGAGAAAAATTAGATCTATTGATACAGTTTACG 423
 358 CAGAGATCCCAATATATGTTTATGCGGATATTTAAATGACATCGGTGAAGTTCCGCA 417
 424 CTTCATGATATTTGTCAGACCGGACGGCCGAAACCTGACATACCAAGAGACAGC 483
 418 TTGCAATTATCATGTTCCGATGACATGACATTCAGTCAATTTCAATTTAAAGGGG 477
 484 GGCCCTCAAGTCTATGATATATCAACCTGGTGTATGACGAAAGCCCGCTTATATG 543
 478 GAAGTGCTTATTAAGATATACCTTATGTTGTTTAAACAATATCTCAAGCTTAAATG 537
 544 CATGTAAACCATCTGACGATATATACAGAAATCAGACGAAAGATTAAGAGCAAAAG 603
 538 CATTAATAGTAAATTAAGACAAATATATCAATATTTCTCTATCCAGCAACAGCAAGTTA 597
 604 ATGGGCGGATTAACCTTCTGCTTTGTCAGGACGCTTGAAGCTGTGGTCTGCGGGG 663
 598 TTGGAAGGTGTATACGATTAACCTTTAGGCAATGAAGAGTACATTTGATTTGCAAGG 657
 664 GATTAATACACCGCTTCCGCTTCTGTCAGAGCTGTTTATTTGAAGAAACATCTAGAGCCG 723
 658 GATTTATCTTCACTAGAGCTTCTGTCAGAGCTTCTGTCAGAGCTTCTGTCAGAGCT 717
 724 GCGGCGGATGAAGCAAGAGGTGTACAGCGCTTTCAAAATTTGGCAAAATATAGAGATA 783
 718 AACATAGATTAAGAAATGATTTAATGAATGATTTATTTATGATGCGGTAATATA 777
 784 CCAAGAGGCGGATGATAGAGAGAGAGCAATTCATTAATGCAATTTACTTCCG 843
 778 CCGATTTGGAATTTAGCTCCGATGATGTCGACATCACTATGATGATTCAGACCGTA 837
 844 ATGTGCAAGCAACCTGAAATCTATTTCCACCACTATGACATCGGCAATCCAAA 903
 838 ATTAATTTAATCAAGAAAGCTTATATTAATGATTTATGCGACATGAATATAGTAC 897
 904 GTAAATTTATTTATGAGAGCTTGAAGCTTTGAGAGCTTAAAGTGTTCGCTTAAGCA 963
 898 TTAAGCTCAGATGATTTAATTAATGAAGAAATGATGATTTTAAGCTGAGAG 957
 964 GAAGAGATTTATGATGATTTAATTA 989
 958 CATATCATATTTAAGAAAGTTGAATGA 983

RESULT 13
 US-08-781-986A-444/C
 ; Sequence 444, Application US/08781986A
 ; Publication No. US2003005443A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5255
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville

STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248BP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 444:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1146 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-444
 Query Match 14.7%; Score 146; DB 2; Length 11466;
 Best Local Similarity 47.5%; Pred. No. 2,9e-32;
 Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

4 ATGTGCAAGCTTATCATTTGGAATCTGTGACCGTTAAACATGATTAAGCAAGAAATG 63
 3688 ATGTGCAAGCTTATCATTTGGAATCTGTGACCGTTAAACATGATTAAGCAAGAAATG 3629
 64 GATTTGCAATTCAGCTGGGGAAGAGGATTTCTATCCGCGCTTACAGCTGGAAC 123
 3628 GATTTGCAATTCAGCTGGGGAAGAGGATTTCTATCCGCGCTTACAGCTGGAAC 3569
 124 AGTGAAGCTGACGGAAGGGCCATGACACAGTACCGCTTATGCGGAGAAAA 183
 3568 TCTTGCACT--GGACGACAGAGCCAAAGCAATATGCTTATTTAGGACAGAAAGAT 3512
 184 CTGGAATAATATATTTTCCGACGCGATTAATGAAGGGGTTTATCTGTGCGGCTT 243
 3511 ATGGAAGGTTTATTTATGATGATGATGATTAAGAAAGGCTTCCATTTCAACAA 3452
 244 TATTTTCCGGGCTATGCGGAGTACGAAAAACGATACGGGAAGATACCGTTCACTTGT 303
 3451 TATTTCCGAGTTATGTTATGATGATGATCAACAAAGCGGACCGGATTAATAG 3392
 304 CCGCATGATTTGTCATGAGGTGCTGTCAGTCTGCACTCTTTGGAAGAGCTTAAGAA 363
 3391 CAAATGAAATGTCATGATGATTTGGATATACAAAGCATTTGAAGATGAAACAA 3332
 364 AAGATTCGATCTTTAAGATTTGAGAAAAATTTGATCTATTTGATACAGTTTACCG 423
 3331 CAGCATCCCAATATATGATGATGATGATTTAATGAACATGCGTGAAGTTCCGCCA 3272
 424 CTTCATGATATTTGTCAGACCGGACGGCCGAAACCTGACATAGAACCAAGAGCAGAC 483
 3271 TTGCAATTATCATGTTCCGATGACATGACATACAGTGAAGTTCAATTAAGAGGCT 3212
 484 GGCCCTCAAGTCTATGATATATCAACCTGGTGTATACGACACAGCCCGCACTTATATG 543
 3211 GAAGTGCTTATTAAGATATATCTTATGTTGTTTAAACAATATCATCCAGACTTAATTTG 3152
 544 CATGTAAACCATCTGACGATATATACAGAAATCAGACGAAAGATTAAGAGCAAAAG 603
 3151 CATTAATAGTAAATTAAGACAAATATATCAATATTTCTCTATCCAGCAACAGCAATTTA 3092

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QY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAGGCTTAGAAGCTGTGCTGCCGGG 663
DB 3091 TTGGAAAGGTGAAGATTGAACCTTTAGGCAATAGAGGATCAATTGGATCCAGGT 3032
QY 664 GATTATACACCGCTTCCCGGTTGTGAGAGCTGTTATTTGAAGAACAATCTAGACCG 723
DB 3031 GGATTTCTTCAACTGAGCGCTTTGTGAAATGCGATTATGAAGAACAATCTGCTCA 2972
QY 724 GCGGCGGATTAAGGAGGTGAACAGCGCTTTTCAAAATTTGGCAAAATATGACGATA 783
DB 2971 AACAAATGATTAAGAAATGAATTTAATGAATGCAATTTATTTAGATGCGTAAATTA 2912
QY 784 CCAAGGCGGAGTGAAGAGGAAGAAAGCAAAATCTATTACCAATATCTCCGTG 843
DB 2911 CCGATTGAATTTGACGTCCGCAATGATGCAATCACTAATGATGATGACAGCCGTA 2852
QY 844 ATGTGCAACGAAGTGAAGTGAATCTATTTCACACATATGACATGCGCAATCCAAA 903
DB 2851 ATAAATTTAACTACAGAAAGCTTATATTAATTAATGAGCAAGCAATGAAATGATGCA 2792
QY 904 GTAAATTTATTTATGAGAAAGCTTGAAGCTTGAAGCTTAAAGTGTTCGCTAAAGCA 963
DB 2791 TTAAGCTCAGAGTATTTAATTAATGAAGAAAGATATGAGATTTTAAAGCTGAGAG 2732
QY 964 GAAGAGATTTCTAGAGCTTAATTA 989
DB 2731 CATATCACTAATTAAGAAAGTTGAATGA 2706

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RESULT 14

US-10-329-624-444/C
Sequence 444, Application US/10329624
Publication No. US20040043037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Pannom

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:
LENGTH: 11466 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 444:
US-10-329-624-444

Query Match 14.7%; Score 146; DB 7; Length 11466;
Best Local Similarity 47.5%; Pred. No. 2,9e-32;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

```

QY 4 ATGTGCAACAGTCTTACATTGGAAGTGTGACCGTAAACATGATTTATGCAAGAAACAATG 63
DB 3688 ATGTGCAACAGTCTTACATTGGAAGTGTGACCGTAAACATGATTTATGCAAGAAACAATG 3629
QY 64 GATTATGATTTATGATGAGTGAAGTGAATTTATGATGAGTGAATTTATGATGAGTGAATTTATG 123
DB 3628 GATTATGATTTATGATGAGTGAAGTGAATTTATGATGAGTGAATTTATGATGAGTGAATTTATG 3569
QY 124 AGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 183
DB 3568 TCTTGCACT--GCAACGACAGGCGCAAGCAATATGCTTTATTTGACAGAGAAACGAT 3512
QY 184 CTTGGAATATATTTATTTGCGGACGCGCATTAATGAAGGCGTTATCTTGCGGCGCTT 243
DB 3511 ATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3452
QY 244 TATTTTCCCGGCTATGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 303
DB 3451 TATTTTCCCGGCTATGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3392
QY 304 CCGCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 363
DB 3391 CAAATGAATTTATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3332
QY 364 AAGATTCGATCTTTAAGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 423
DB 3331 CAAGCATCCCAATATCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3272
QY 424 CTTCAGTGAATTTATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 483
DB 3271 TTGCATTTATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3212
QY 484 GGCCTCAAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 543
DB 3211 GAAGTGTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3152
QY 544 CATGTACCAATCTGACAGCAATATTAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCA 603
DB 3151 CATGTACCAATCTGACAGCAATATTAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCA 3092
QY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAGGCTTAGAAGCTGTGCTGCCGGG 663
DB 3091 TTGGAAAGGTGAAGATTGAACCTTTAGGCAATAGAGGATCAATTGGATCCAGGT 3032
QY 664 GATTATACACCGCTTCCCGGTTGTGAGAGCTGTTATTTGAAGAACAATCTAGACCG 723
DB 3031 GGATTTCTTCAACTGAGCGCTTTGTGAAATGCGATTATGAAGAACAATCTGCTCA 2972
QY 724 GCGGCGGATTAAGGAGGTGAACAGCGCTTTTCAAAATTTGGCAAAATATGACGATA 783
DB 2971 AACAAATGATTAAGAAATGAATTTAATGAATGCAATTTATTTAGATGCGTAAATTA 2912
QY 784 CCAAGGCGGAGTGAAGAGGAAGAAAGCAAAATCTATTACCAATATCTCCGTG 843
DB 2911 CCGATTGAATTTGACGTCCGCAATGATGCAATCACTAATGATGATGACAGCCGTA 2852
QY 844 ATGTGCAACGAAGTGAAGTGAATCTATTTCACACATATGACATGCGCAATCCAAA 903
DB 2851 ATAAATTTAACTACAGAAAGCTTATATTAATTAATGAGCAAGCAATGAAATGATGCA 2792
QY 904 GTAAATTTATTTATGAGAAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 963

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:54:08 ; Search time 452 Seconds

(without alignments)
5138.006 Million cell updates/sec

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Perfect score: 996
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Gapop 10.0, Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA-New*

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13: /cgn2_6/ptodata/1/pubpna/US18_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	16.0	990	US-10-793-626-413	Sequence 413, App
2	159	16.0	2975	US-10-793-626-345	Sequence 345, App
3	159	16.0	4114	US-10-793-626-4184	Sequence 4184, App
4	93	9.3	975	US-11-074-176-367	Sequence 367, App
5	83.8	8.4	975	US-11-074-176-369	Sequence 369, App
6	38.8	3.9	720	US-10-750-185-59863	Sequence 59863, A
7	38.8	3.9	720	US-10-750-623-59863	Sequence 29811, A
8	36.2	3.6	1272	US-11-096-568A-29811	Sequence 29811, A
9	35.8	3.6	583	US-09-925-065A-392869	Sequence 392869, A
10	35.4	3.6	419	US-09-925-065A-654182	Sequence 654182, A
11	35.4	3.6	419	US-09-925-065A-654183	Sequence 654183, A
12	35.4	3.6	5901	US-10-932-182A-2969	Sequence 2969, App
13	35.4	3.6	5901	US-10-932-182A-2969	Sequence 2969, App
14	35	3.5	961	US-11-072-175-102	Sequence 102, App
15	34.6	3.5	583	US-09-925-065A-392868	Sequence 392868, App
16	34.4	3.5	4429	US-10-753-195-9	Sequence 9, App11
17	34.2	3.4	583	US-09-925-065A-392870	Sequence 392870, A
18	34.2	3.4	1835	US-09-925-065A-45228	Sequence 45228, A
19	34.2	3.4	1835	US-09-925-065A-45229	Sequence 45229, A
20	34.2	3.4	1835	US-09-925-065A-45230	Sequence 45230, A

21	34	3.4	601	US-09-925-065A-348226	Sequence 348226, App1
22	34	3.4	193084	US-11-121-086-82	Sequence 82, App1
23	33.8	3.4	670	US-09-925-065A-556802	Sequence 556802, App1
24	33.6	3.4	523	US-09-925-065A-155341	Sequence 155341, App1
25	33.6	3.4	556	US-09-925-065A-770702	Sequence 770702, App1
26	33.4	3.4	572	US-09-925-065A-29870	Sequence 29870, A
27	33.4	3.4	580	US-09-925-065A-321496	Sequence 321496, A
28	33.4	3.4	653	US-09-925-065A-96912	Sequence 96912, A
29	33.4	3.4	659	US-09-925-065A-510272	Sequence 510272, A
30	33.4	3.4	958	US-09-925-065A-713894	Sequence 713894, App1
31	33.4	3.4	958	US-09-925-065A-713895	Sequence 713895, App1
32	33.4	3.4	1197	US-10-750-185-62875	Sequence 62875, A
33	33.4	3.4	1197	US-10-750-623-62875	Sequence 62875, A
34	33.4	3.4	1217	US-09-925-065A-686875	Sequence 686875, A
35	33.4	3.4	2830	US-09-925-065A-669245	Sequence 669245, App1
36	33.4	3.4	2830	US-09-925-065A-669246	Sequence 669246, App1
37	33.2	3.3	629	US-09-925-065A-346097	Sequence 346097, App1
38	33.2	3.3	645	US-09-925-065A-860511	Sequence 860511, App1
39	33.2	3.3	661	US-09-925-065A-690516	Sequence 690516, App1
40	33.2	3.3	2037	US-10-932-182A-1230	Sequence 1230, App
41	33.2	3.3	2037	US-10-932-182A-1230	Sequence 1230, App
42	33.2	3.3	156297	US-11-121-086-65	Sequence 65, App1
43	33	3.3	393	US-09-925-065A-148412	Sequence 148412, App1
44	33	3.3	499	US-09-925-065A-845854	Sequence 845854, App1
45	33	3.3	566	US-09-925-065A-828854	Sequence 828854, App1

ALIGNMENTS

RESULT 1
US-10-793-626-413 Application US/10793626
Sequence 413, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164, 258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 413
LENGTH: 990
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-413

Query Match 16.0%; Score 159; DB 8; Length 990;
Best Local Similarity 49.8%; Pred. No. 2e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
2 ATATGTCACAGCTTACATGGAACCTGCGGCAACATGTAATGCAAGACAA 61
8 ATATGTCACAGCTTACATGGAACCTGCGGCAACATGTAATGCAAGACAA 67
62 TGAATTTGCAATTCAGCTGCGGCAACAGGCTGATTCATTCGCGCGCTTACAGCTGA 121
68 TGAATTTGCAATTCAGCTGCGGCAACAGGCTGATTCATTCGCGCGCTTACAGCTGA 127
122 AACTGGAATATATATTTGCGGCAACAGGCTGATTCATTCGCGCGCTTACAGCTGA 181
128 AATTGATCTAGATTCAGATGCTGCTT---GATATGCTTTTGTGGAACAAATTTAA 184
182 AACTGGAATATATATTTGCGGCAACAGGCTGATTCATTCGCGCGCTTACAGCTGA 241
185 AAGTAGACCTTATGATGCTGATTAACGAAAAGGTTAGCTATTTGCAACC 244


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; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4184
; LENGTH: 4114
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-793-626-4184

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Query Match      16.0%; Score 159; DB 8; Length 4114;
Best Local Similarity 49.8%; Pred. No. 4e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

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QY 2 ATATGTCACAAAGTCTTACATGGAAACGTGACCGTAAACATGATATGCAAGAACAA 61
DB 1626 ATATGTCACAAAGTCTTACATGGAAACGTGACCGTAAACATGATATGCAAGAACAA 1685
QY 62 TGGATTTTGGCATTTGACGTGGGACACAGAGTATCTCTATCCGCGCCGTACAGTGA 121
DB 1686 TGGATTTTGGCATTTGACGTGGGACACAGAGTATCTCTATCCGCGCCGTACAGTGA 1745
QY 122 ACAGTGAAGCTGACGGAAGGCGCCATCAGACAGTACCGCTTATCGGTATGGGAGAA 181
DB 1746 AATTGATCTTACATTCAGACATGCGCTT---GAATATGTTTGTGGAAACAAATTGAA 1802
QY 182 AACTGGAATATATATTTATGCGGACGCGATTAATGAAGCGGTTATCTTGCGCGCC 241
DB 1803 AAGTGAAGCTTATGATTTGTTGATGATTAACGAAAGGTTAGCTTATTTGGAACC 1862
QY 242 TTTATTTTCCGGGCTATGCGGAGTACGAAACGATACGGAAGTACCGTTCACTTG 301
DB 1863 ATTACTTCACTGGTGAAGCTCATACAGTACCCATTAAGTATGTTTAACTTAG 1922
QY 302 TCCGCGCATGAGTTTGTGACATGGGTGCTGCTGCTGCTGCTGCTTGGAAAGCGTAAAG 361
DB 1923 CACCTGAGAGATTATGTTGTTGGTTTATGTTTAAATGAATATGCGAATTAAAC 1982
QY 362 AAAAGATTCGANTCTTAACGATTTGAGAGAAATATGATCTATTTGATACAGTTTAC 421
DB 1983 AAAAGATTCGANTCTTAACGATTTGAGAGAAATATGATCTATTTGATACAGTTTAC 2042
QY 422 CGCTTCACTGATATTTGTGACACCGGCGGCGGAAACCTGACATAGAACCAAGAGCAG 481
DB 2043 CTTTACATTTTCACTGATATTTGTGACACCGGCGGCGGAAACCTGACATAGAACCAAG 2102
QY 482 ACGGCTCAAAAGTCTATGATTAATCAACCTGTGTATGACGAAACCGCCGACTTATAT 541
DB 2103 GCTTATATATAGTTAAAGATTAATATGTTTACATACCTTAACAAATGAACTTAATAGAT 2162
QY 542 GGCATGTATACCAATGTGACGAAATATACAGAAATGACACGGAACAAATTAAGAGCAAG 601
DB 2163 GGCATGTATGTAACTTAAGAAATTAAGCTTTTAAACGCAAGAAATCAACCAATCAAT 2222
QY 602 AGATGGCGGATTAAGCCCTTCTGCTTTGGCCAGGCTTGAAGACTTGGTCTGCGCG 661
DB 2223 TAAATGTAAGTGTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2282
QY 662 GGGATTAATACACCGCTTCCGGTGTGCAAGCTGTTTATTTGAAAGAACATCTAGAC 721
DB 2283 GTGTGTATACGTCACAGATGCTTTTATACGCGTACATATTTAAGAACACCAATACCT 2342
QY 722 CGGGCGCGGATGAAGCAAGGTGTAAGCGGCTTTTCAAAATTTGGCAAAATATGACGA 781
DB 2343 GTTCCCATTAATGAAGATGAAGATTAATGAATGTTTAAAGTTCTAATAATCAGTACGTA 2402

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QY 782 TACCAAGGCGCGAGTATGATTAACGGAAGAGCAAAATTCATTATACGAATATACCTCCG 841
DB 2403 TCCCTCAAGGTGACAGTTAT---CGATGCCAATTAATATATATACATATACATATCATTTG 2459
QY 842 TGAATGTCACAAAGTGAAGAACTGAAACTATTTTCCACACATATGACATGCGCAATCCAA 901
DB 2460 TGAATGTCACAAAGTGAAGAAAGTATTTATATTAAGCTTACCTTACATCAAAATTTTCA 2519
QY 902 AAGTAAATTTATTTATGATA 920
DB 2520 AATTAATAATTAAGTAAAG 2538

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RESULT 4
US-11-074-176-367

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```

; Sequence 367, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kleenhamer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altemann, Eric
; APPLICANT: McAllister, Olivia
; APPLICANT: Petil, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 367
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(975)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 892; bsba
; US-11-074-176-367

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Query Match      9.3%; Score 93; DB 12; Length 975;
Best Local Similarity 46.4%; Pred. No. 2e-16;
Matches 340; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

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QY 197 TATTTGCGGAGGAGTAAATGAAGCGGTTATCTTGCGCGCCTTATTTCCGGCT 256
DB 188 TATATTTGAGCGCTTAAATGAAGGTTATGATAGCGGAGCTCAATCAATCCAGGAA 247
QY 257 ATGCGAGTACGAAAGAAACGATACGGAAGTACCGTTCACTTGTCCGATGAGTTTG 316
DB 248 ATGCTACATATTAAGAGAGAAA---GAAATTAAGTAAATATGCTTCTTGAATTTCA 304
QY 317 TGAATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
DB 305 TCCCTGATTTTGAAGCAGGTGACATATTAAGCAAGTAAAGATTTTACTAGCAGAA 364
QY 377 TAAAGATTTGAGAGAAATTAATGATCTATTTGATACGTTTACCGTTACTGAGATAT 436
DB 365 TCAATCGCGCGATTTTAAATTTTACGCGAGAAATGCAAGGCTCTCTTCTTCACTGGCTTA 424
QY 437 TGTCAACCGGACGCGCGGAAACCTGACGATAGAACCAAGAGCAGCGGCTCAAAGTCT 496
DB 425 TTGCAAGTAAAGACGAGTACATTAAGTTGTTGAAACAGCAAGATGAGATGATATTT 484
QY 497 ATGATTAATCAACTGTGTGCTATGACAGACGCGGCACTTATATGCGATGTAACAATC 556
DB 485 ATGATTAATCAAGTTGGCTGTCTTAATTAATATCACAATTTCCAAAGCAATTAATTAAT 544

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Oy	557	TCGACGACATATATCAGAGAAATCAGACCGAGCAATTTAGAGAGCAAAAGATGGCGGATTG	616
Db	545	TAAATATCTATGCTACGATCTATCTCCAAAATGCTTAAATAATATCTTCAATTAAGTAA	604
Oy	617	CCCTTTCTGCTTTTGGCCCAAGGCTTAGAAGACTGTGGTGTGCGCGGGGATTATACACGC	676
Db	605	ATATGCTGGCTACAGCCGCTGATTAAGGCTTCACAACTTACAGAGTGAATGATTTCTG	664
Oy	677	CTTCCCGGTTTGTCTAGAGCTGTATTATTGAAAGACATCTAGACCGCGCGCGATGA	736
Db	665	AATACAGTTTGTCTAGAGTAGGCTTCAATTAATTAATCTCCAAATTTGCTGAACCGAAG	724
Oy	737	CGAAAGTGTTAACAGCGCGCTTTTCAAATTTTGGCAAAATATGACGATACCAAGGGCGCAG	796
Db	725	AAGAAAATATTTATATCTTACTTACTTCCACATTTTACTTCGGTTGAACAACAAAAGGACTGG	784
Oy	797	TGATATACGGAAGAGACGAATTCATTTATATGCGCAATATATCTTCGATGTGCAAGAA	856
Db	785	ATGAAGTTGTGTCCAAACTCATTTGAATATATCAATTTATTTCTGATGGAATACTAATTGAGCA	844
Oy	857	CTGGAATCTACTATTTTCCACCACTATGACAAATCGGAAATCCAAAAGTAAATTTATTTC	916
Db	845	AAGGATATTTTCTACTACACCACTTATTCAAAACAAACAAATTTAACGTTGTTGATGAAATA	904
Oy	917	ATGAAGACCTTGA	929
Db	905	AAGAGATCTAGA	917

RESULT 5
 US-11-074-176-369
 Sequence 369, Application US/11074176
 Publication No. US20050250135A1
 GENERAL INFORMATION:
 APPLICANT: Kleenhammer, Todd R.
 APPLICANT: Russel, William M.
 APPLICANT: Altermann, Eric
 APPLICANT: McAuliffe, Olivia
 APPLICANT: Peril, Andrea, Azcarate
 TITLE OF INVENTION: Nucleic Acid Sequences Encoding
 TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
 FILE REFERENCE: 5051-694
 CURRENT APPLICATION NUMBER: US/11/074, 176
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: 60/551,161
 PRIOR FILING DATE: 2004-03-08
 NUMBER OF SEQ ID NOS: 381
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 369
 LENGTH: 975
 TYPE: DNA
 ORGANISM: Lactobacillus acidophilus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(975)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)...(0)
 OTHER INFORMATION: ORF 1078; bshb
 US-11-074-176-369

	Query Match	8.4%	Score 83.8;	DB 12;	Length 975;
	Best Local Similarity	45.4%;	Pred. No. 8.9e-14;		
	Matches 341;	Conservative	0;	Mismatches 407;	Indels 3; Gaps 1.
QY	181	AAACTTGGAAATATATATATTTTCCGACGGCATTAATGAAAGCGTTATCTGTGCGCG	240		
DB	172	AATGATGATTAATCCATTAATTAATGATGATGCAATTAATGAAAGCGCTTGATTTGCAGGA	231		
QY	241	CTTATATTTTCCGGCGCATGCGGAGTACGAAAAAGATACGGGAAGATACCGTTGACATT	300		
DB	232	TTAAATTTTTCAGG--TCTATATCATTTCTTTCTTAAATTCGAAAGGTAGAAGATATT	288		

Oy	301	GTCCGCGATGAGTTTGATGCAAGGGTGTGTCAGTCTGTCAGTCTTTGGAAAGCGTAAA	360
Db	289	GCTTCTTTGAATTAATGCACTACTATTAAAGTAATTTGTAAATTAATGCAAGTGTAAA	348
Oy	361	GAAGAGATTGCATCTTTAAGCATGTGTAGAGAAAAAATTAGATCTATTGGATACAGTTTA	420
Db	349	GAATCTTAGATATAGCAAAATTTTAAATTTATGTAGCTTTTCAGCAAAATTTATCCGCAGCT	408
Oy	421	CCGCTTCACTGATATATGTGCAAGCCGAGCGGGCCGAAACCTGACGATAGAACCAAGCA	480
Db	409	GATTTCATTTGATTTTAAGTATTAAGCTGTAGAGTATCGTAGTTGAATCAACCAAT	468
Oy	481	GACGCGCTCAAAAGTCTATGATATCAACCTGTGTCTCATGACGAACAGCCCGACTTTATA	540
Db	469	TCAAGTTTACATTTATTAATGATATCAAGTAAATGTCTTTACTMAACAATCCGAAATTTCCG	528
Oy	541	TGGCATGTATACCAATCTGCAAGCATATACAGAAATCAAGCCGAAGCAATTAGAGACAA	600
Db	529	GATCATTTAATTAATTAATTAAGTACACACCCACGTTACTCCACATTAATCTTAAGAAATCA	588
Oy	601	GAAATGGGGCGAATTAGCCCTTCTGCTTTTGGCCAAAGCTTAGAACTGTGTGGTCCCG	666
Db	589	TTGTGTTCTTAATGTGTGATCTTATTTATTAATATAGTAGAGGCTTAGGTACTCAACCACTTACT	648
Oy	661	GGGGATTTATACACCGCTCTCCGGGTTTGTGCAAGCTGTTATTTGAAAGAATCTAGAG	720
Db	649	GGTGAATAGATTCTAGACTCGATTTTGTTAAGGAGCTTTTGTCTTGGCACACATCCA	708
Oy	721	CCGGCGCCGATGAACAAGAAAGTGTAAACAGCCGCTTTCAAAATTTGGCAAAATAGACG	780
Db	709	CAAGGAAAAAATGAAGTGGAAAAATGTCTAATTAATTTCCATATTCGATTCAGTAGAA	768
Oy	781	ATACCAAAAGGGCGCATGTATTAACGGAAGAAACGAAATTCATATTACCAATTAATCTTC	840
Db	769	CAATCTGATGGTTTATGATGATGAAAGTATGAAATTAATGCTATGATATATATATGATACGAT	828
Oy	841	GTGATGTGCACGAACCTGGAACCTACTATTTCACCACTATGACCAATCGGCAAAATCAA	900
Db	829	TGTATGAACCTTGAATTAAGGTATTTTGTACTTTACTACTATATGACAAATATCGGATTAAT	888
Oy	901	AAGTAAATTTATTTATGAAAGACTTACT	931
Db	889	GCAGTAGATATGCAATTAAGCAATTTAAATT	919

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RESULT 6
US-10-750-185-59863/c
; Sequence 59863, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64822
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59863
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Bovine 19866881284323
US-10-750-185-59863

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Best Local Similarity 57.4%; Pred. No. 0.7; Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 824 ATACGCAATTAATCTCCGATGATGCAACGAACTGAACTATTTCCACCACTATG 883
DB 262 ATACCAATGTTGTCTATCTATTTATATACGAAAGTATATTTTATCTATATC 203
QY 884 ACAATGGCAATCCAAAAGTAAATTTATTTATGTAAGACCTTGCTTTGAGCCTA 943
DB 202 ACCTGGGTAAATAGAAATGCAATTTTATTCAGTTGTGCTAACTGGTTCAACTC 143
QY 944 AA 945
DB 142 AA 141

RESULT 7

US-10-750-623-59863/c
; Sequence 59863, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59863
LENGTH: 720
TYPE: DNA
ORGANISM: Bovine 19866881284323
US-10-750-623-59863

Query Match
Best Local Similarity 3.9%; Score 38.8; DB 8; Length 720;
Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 824 ATACGCAATTAATCTCCGATGATGCAACGAACTGAACTATTTCCACCACTATG 883
DB 262 ATACCAATGTTGTCTATCTATTTATATACGAAAGTATATTTTATCTATATC 203
QY 884 ACAATGGCAATCCAAAAGTAAATTTATTTATGTAAGACCTTGCTTTGAGCCTA 943
DB 202 ACCTGGGTAAATAGAAATGCAATTTTATTCAGTTGTGCTAACTGGTTCAACTC 143
QY 944 AA 945
DB 142 AA 141

RESULT 8

US-11-096-568A-29311
; Sequence 29311, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
PRIOR FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29311
LENGTH: 1272

TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1272)
OTHER INFORMATION: Ceres Seq. ID no. 4809357
US-11-096-568A-29311

Query Match
Best Local Similarity 3.6%; Score 36.2; DB 9; Length 1272;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 149 AGACAGATACCGCTTTATCGGTATGGGAGAAAATTGAAATATATTATTTCCGACG 208
DB 419 AGACTGACCTTGGTTCTCGATGATGATGATGATGATGATGATGATGATGATG 478
QY 209 GCATTAATGAAAGCGCTTATCTTTGCGCGCTTATTTTCCGCGCTATGCG 261
DB 479 GCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 531

RESULT 9

US-09-925-065A-392869/c
; Sequence 392869, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 392869
LENGTH: 583
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-392869

Query Match
Best Local Similarity 3.6%; Score 35.8; DB 6; Length 583;
Matches 88; Conservative 1; Mismatches 88; Indels 0; Gaps 0;

QY 802 ACGAAGAAGCAAAATTCATTAATGCAATATATCTCCGATGATGCAACGAACTGCA 861
DB 341 ATGGAAGAAGCTTAATGATATATTAATCAAGTAAAGAAAGAAAGATGTAATG 282
QY 862 AACTACTATTTCCACCACTATGACATCGCAATTCAGAAAGTAAATTTATTTCA 921
DB 281 CTGATTAATGATTCACATATGATGATGATGATGATGATGATGATGATGATG 222
QY 922 GACCTGACTGTTGGAGCCTTAAGTGTGTTTCCGCTAAAGCAAGAGATTTTCAT 978
DB 221 GATAGTGTTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 165

RESULT 10

US-09-925-065A-654182
; Sequence 654182, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.

```

; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 654182
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-654182

Query Match
Best Local Similarity 3.6%; Score 35.4; DB 6; Length 419;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```

QY 333 AGCTGTCAGTCTTGGAGACGTAAAGAAAGATTGATCTTAAAGATTGAGAA 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 AGATTACAGAAATTTAAGAAACAGAAATTTAAGATATTAATCGAACATTTTATGGA 303

QY 393 AAAATTAGATCTATTGATACAGTTTACCGCTTCACTGATTTGTA 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 TAAATTGATGACAGATTTATTTCTTCCATCTGATTTGTTA 352
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```

RESULT 11
US-09-925-065A-654183
; Sequence 654183, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 654183
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-654183
```

```

Query Match
Best Local Similarity 3.6%; Score 35.4; DB 6; Length 419;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```

QY 333 AGCTGTCAGTCTTGGAGACGTAAAGAAAGATTGATCTTAAAGATTGAGAA 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 AGATTACAGAAATTTAAGAAACAGAAATTTAAGATATTAATCGAACATTTTATGGA 303
```

```

QY 393 AAAATTAGATCTATTGATACAGTTTACCGCTTCACTGATTTGTA 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 TAAATTGATGACAGATTTATTTCTTCCATCTGATTTGTTA 352

RESULT 12
US-10-932-182A-2969
; Sequence 2969, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2969
; LENGTH: 5901
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2969

Query Match
Best Local Similarity 3.6%; Score 35.4; DB 7; Length 5901;
Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```

QY 693 AGCTGTTATTGTAAGACATCTAGACCGCGCCGATGAACGAAGGTGAACAGC 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 894 AGCTTATACAAAGAAATGATTTGATTTGCGCTACAGTGCAGGTAAACAGA 953

QY 753 CGCTTTCAATTTTGGCAATATGACGATACCAAGGGCGGAGTAAACGAAGAGA 812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 954 CGTTCACACTTACGATATTAACAGGTAAACAGTTCTCCGTATCAACGAGAAAA 1013

QY 813 CGAAATTCATTATACGCAATATATCTCCGTATGTGCAACGAAC 857
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 CGAAATTCATTATACGCAATATATCTCCGTATGTGCAACGAAC 1058
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```

RESULT 13
US-10-932-182A-2969
; Sequence 2969, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2969
; LENGTH: 5901
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2969
```

```

Query Match
Best Local Similarity 3.6%; Score 35.4; DB 7; Length 5901;
Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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```

QY 693 AGCTGTTATTGTAAGACATCTAGACCGCGCCGATGAACGAAGGTGAACAGC 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 894 AGCTTATACAAAGAAATGATTTGATTTGCGCTACAGTGCAGGTAAACAGA 953
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QY 753 CGCTTTCAATTTGGCAATATGACGATACCAAGGGCGCAGTGTATACGGAAGAA 812
DB 954 CGTTGACGACTTACGATATTAAACAGGTAACGTTTCCTGATCAACGAGAAA 1013
QY 813 CGAATTCATTATACGCAATATATCTCCGTGATGTGCAAGAA 857
DB 1014 CGAATTCATTATACGATATGATGTTCAAGTTGCTACTAGTAC 1058

RESULT 14

US-11-072-175-102
; Sequence 102, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; PRIOR FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-102

Query Match 3.5%; Score 35; DB 9; Length 961;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 107; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 293 TTCAATGTCTCCGATGATGTTTGACATGGTGTCTGATCTGTCACTTTGGAG 352
DB 466 TTAACACAGTTCATGAAAGTTGGCTTCTGTTGATGTTGCTGCTGGAACC 525
QY 353 ACGTAAAGAAATTCATCTTAACATGTAAGAAAAATTAATGATCTATGATA 412
DB 526 AGGAGACGACATTTAGATGATGTTCTGTCTTCACTGAAATTTCTATTCATTGAGA 585
QY 413 CAGTTTACCGCTTCACTGATATTTGTGACCCGACGGCCGAAACCTGACATAGAAC 472
DB 586 CATTTCCTTATCCACGATATTTTGTGACCTGTCATCATGAATACCCCTTAGGAA 645
QY 473 CAAGACGACGGCTCAAGTCTATGATATCAACTGGTGTATG 519
DB 646 AATAAGATTACTGCAAAATTAAGAAACGAAACGAACTGATATG 692

RESULT 15

US-09-925-065A-392868/c
; Sequence 392868, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392868
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-392868

Query Match 3.5%; Score 34.6; DB 6; Length 583;
Best Local Similarity 49.7%; Pred. No. 10;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 802 ACGAAGAAGCAAAATTCATTATGCAATATATCTTCGTGATGTGCAAGAACTGGA 861
DB 341 ATGGAAGAGCTTAATGATATTTACAAAGTAAAGAACATCTGAAAGCTGCATA 282
QY 862 AACTATATTTCCACCACTATGACATCGCAATCCAAAATTAATTTATTCATGAA 921
DB 281 CTGATATGATTCACATATATGACATTCAGAAAACAAAACATGTAATAGTAAAA 222
QY 922 GACCTTGACTGTTTGAGCTTAAAGTGTTCCTGCTAAAGCAAGAGCTATTCAT 978
DB 221 GATCAGTGTGTCAGGGAACCGGGGAGTGAACAGGTGCGCACAGGATTCCT 165

Search completed: March 18, 2006, 12:06:10
Job time : 453 secs

GenCore version 5.1.7
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OW nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:44:38 ; Search time 5413 Seconds
(without alignments)
10459.279 Million cell updates/sec

Title: US-10-812-387-1

Sequence: 1 catcagtcgacgaagctctac.....atgagcttaataagatcc 996

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pr: *
9: gb_to: *
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11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_hlg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	996	6	CS128791
2	978.8	98.3	23351	1	CS128791 Sequence
3	978.8	98.3	203901	1	D45912
4	440	44.2	110000	1	BSUB00021
5	440	44.2	110000	1	AE017333_40
6	439.8	44.2	110000	1	CP000002_40
7	293.2	29.4	110000	1	AX433304
8	293.2	29.4	110000	1	AE017225_35
9	293.2	29.4	110000	1	AE017334_35
10	290.6	29.2	110000	1	AE017355_35
11	274.6	27.6	304708	1	AE017001
12	273.8	27.5	287765	1	AE017276
13	233.6	23.5	280050	1	AE017276
14	233.6	23.5	280050	1	AL591975
15	232.6	23.4	990	6	AX641665
16	232.6	23.4	990	6	AX413775
17	196.4	19.7	1087	1	AX415691
18	196.4	19.7	1087	6	CP020191
					Q0874237

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20	177	17.8	10647	1	AE006413	AE006413 Lactococ
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22	167.6	16.8	110000	1	AP008934_01	Continuation (2 of
23	162.2	16.3	110000	1	CP000029_02	Continuation (3 of
24	159	16.0	990	6	AR483788	AR483788 Sequence
25	159	16.0	990	6	AX141691	AX141691 Sequence
26	159	16.0	2975	1	AF269303	AF269303 Staphyloc
27	159	16.0	2975	6	AR485259	AR485259 Sequence
28	159	16.0	2975	6	AX144623	AX144623 Sequence
29	159	16.0	4114	1	AF270144	AF270144 Staphyloc
30	159	16.0	4114	6	AR486098	AR486098 Sequence
31	159	16.0	4114	6	AX145462	AX145462 Sequence
32	157.4	15.8	300242	1	AE016745	AE016745 Staphyloc
33	149	15.0	298050	1	AL935261	AL935261 Lactobaci
34	146	14.7	999	6	AX619460	AX619460 Sequence
35	146	14.7	11466	6	AR354326	AR354326 Sequence
36	146	14.7	11466	6	AR355882	AR355882 Sequence
37	146	14.7	110000	1	BA000017_03	Continuation (4 of
38	146	14.7	110000	1	BA000018_03	Continuation (4 of
39	144.4	14.5	110000	1	CP000046_02	Continuation (3 of
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45	120.8	12.1	110000	1	AP006716_02	Continuation (3 of

ALIGNMENTS

RESULT 1
LOCUS CS128791 996 bp DNA linear PAT 02/AUG-2005
DEFINITION Sequence 1 from Patent WO2005066336.
ACCESSION CS128791
VERSION CS128791.1 GI:71794812
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Council of Scientific and Industrial Research (IN); University of
York (GB)

FEATURES

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1..996
/organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/db_xref="taxon:1423"

ORIGIN

Query Match 100.0%; Score 996; DB 6; Length 996;
Best Local Similarity 100.0%; Pred. No. 1.9e-259;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATATGTCACAGCTTCTTACATTGGAACCTGTCACCGTTAAATGATATGACAGACACA 60
1 CATATGTCACAGCTTCTTACATTGGAACCTGTCACCGTTAAATGATATGACAGACACA 60
DB 1 CATATGTCACAGCTTCTTACATTGGAACCTGTCACCGTTAAATGATATGACAGACACA 60
QY 61 ATGATTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 120
61 ATGATTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 120
QY 121 AACAGTGAAGTGAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
121 AACAGTGAAGTGAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 AACAGTGAAGTGAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
121 AACAGTGAAGTGAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 AAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240
181 AAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240

Db	181	AAACTGGAAATATATATATTTTCGCCAGCCGACCTTAATGAAAGCGGTTTATCTTGTCGGCG	240
Oy	241	CTTTATTTTTCGGGGCTATGCGGAGTACGAAAAACGATACGGGAAGATACCGTTCACTT	300
Db	241	CTTTATTTTTCGGGGCTATGCGGAGTACGAAAAACGATACGGGAAGATACCGTTCACTT	300
Oy	301	GTCCCGCATGAGTTTGTGACATGGGGCTGTCAGTCTGCAGTCTTTGGAAACGTTAAA	360
Db	301	GTCCCGCATGAGTTTGTGACATGGGGCTGTCAGTCTGCAGTCTTTGGAAACGTTAAA	360
Oy	361	GAAGAATTCGATCTTTAACGATTGTAGAAAAAATTAGATCTATTGGATACAGTTTAA	420
Db	361	GAAGAATTCGATCTTTAACGATTGTAGAAAAAATTAGATCTATTGGATACAGTTTAA	420
Oy	421	CCGCTTCACTGATATTTGTCAACCGCGACGGGCCGAAAACCTGACATGAAACCAAGACA	480
Db	421	CCGCTTCACTGATATTTGTCAACCGCGACGGGCCGAAAACCTGACATGAAACCAAGACA	480
Oy	481	GACGGCCCTCAAGCTATGATATCAACTGGTGTCTATGACGAACAGCCCCGACTTTATA	540
Db	481	GACGGCCCTCAAGCTATGATATCAACTGGTGTCTATGACGAACAGCCCCGACTTTATA	540
Oy	541	TGGCATGTAAACCAATCTGACGCAATATACAGGAATCAACCGAACAATTAGAGCAAA	600
Db	541	TGGCATGTAAACCAATCTGACGCAATATACAGGAATCAACCGAACAATTAGAGCAAA	600
Oy	601	GAGATGGGCGGATTTAGCCCTTTCTGCTTTGGCCAAAGCTTAGAAGCTGTGCTGCGCG	660
Db	601	GAGATGGGCGGATTTAGCCCTTTCTGCTTTGGCCAAAGCTTAGAAGCTGTGCTGCGCG	660
Oy	661	GGGGATTTATACACCGCTTCCCGGTTTGTCAAGCTGTTTATTGAAAGACATCTAGAG	720
Db	661	GGGGATTTATACACCGCTTCCCGGTTTGTCAAGCTGTTTATTGAAAGACATCTAGAG	720
Oy	721	CCGGCGGCCGATGAACGAAAGGTGTACAGCCGCTTTCAAAATTTGGCAAAATAGACG	780
Db	721	CCGGCGGCCGATGAACGAAAGGTGTACAGCCGCTTTCAAAATTTGGCAAAATAGACG	780
Oy	781	ATACCAAAAGGGGCGAGTGTAAACGGAAGAAAGCAAAATTCATTATACGGAATATCTCC	840
Db	781	ATACCAAAAGGGGCGAGTGTAAACGGAAGAAAGCAAAATTCATTATACGGAATATCTCC	840
Oy	841	GTGATGTGCACGAAACTGGAACCTACTATTTCCACCACTATGACAAATGGCAAAATCCAA	900
Db	841	GTGATGTGCACGAAACTGGAACCTACTATTTCCACCACTATGACAAATGGCAAAATCCAA	900
Oy	901	AAAGTAAATTTATTTTCATGAAAGCTTGACTGTTTGGAGCCTTAAAGTGTTTCCGCTAAA	960
Db	901	AAAGTAAATTTATTTTCATGAAAGCTTGACTGTTTGGAGCCTTAAAGTGTTTCCGCTAAA	960
Oy	961	GCAGAAAGAGATATTCATGAGCTTATTAATTAAGGATCC	996
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DEFINITION	partial and complete cds.				
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VERSION	human; pdp; nucK; dra; deor; yxxB; yxwE; yxeO; yxep; yxoO; yxen;				
KEYWORDS	yxEI; yxel; yxgC; yxel; yxwH; yxeg; yxFf; yxBE; yxwC; yxwG; yxwM; yxDk; hypothetical DNA-binding protein; deoxyribose-phosphate aldolase; pyrimidine nucleoside transport protein; pyrithidine nucleoside phosphorylase; putative histidine				
SOURCE	Bacillus subtilis				
ORGANISM	Bacillus subtilis				
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus:				
AUTHORS	1 (sites)				
	Yoshida,K., Sano,H., Miwa,Y., Ogasawara,N. and Fujita,Y.				

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 ACCESSION Z99124 AL009126
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 KEYWORDS
 SOURCE
 ORGANISM
 AUTHORS
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 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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FEATURES
 source
 COMMENT
 On Jul 7, 2003 this sequence version replaced gi:2636442.
 This entry contains data from release R16.1 of the Subtilist
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51519 GTCCGCGATGAGTTTGTGACATGGGTGCTGTCACTGTGTCTTGTGAAGACGTAA 51460
361 GAAAATTCGATCTTAAACGATTTGAGGAAAAATTTAGTCTATTGGATACAGTTT 420
51459 GAAAATTCGATCTTAAACGATTTGAGGAAAAATTTAGTCTATTGGATACAGTTT 51400
421 CCCTTCATCTGATATTTGTCAACGCGGCGGAAACCTGACGATAGAACCAAGACA 480
51399 CCCTTCATCTGATATTTGTCAACGCGGCGGAAACCTGACGATAGAACCAAGACA 51340
481 GACGCGCTCAAGTCTAGATTAATCAACTGTGTGTATGACGAAAGCCCGACTTTATA 540
51339 GACGCGCTCAAGTCTAGATTAATCAACTGTGTGTATGACGAAAGCCCGACTTTATA 51280
541 TGGCAGTAAACCAATTCGACGAAATTAACGAAATGACCCGAAACATTAAGAGCAAA 600
51279 TGGCAGTAAACCAATTCGACGAAATTAACGAAATGACCCGAAACATTAAGAGCAAA 51220
601 GAGATGGGCGGATTAAGCCCTTCTGCTTTGGCGCAAGGCTTGAAGACTGTTGGCTGCGG 660
51219 GAGATGGGCGGATTAAGCCCTTCTGCTTTGGCGCAAGGCTTGAAGACTGTTGGCTGCGG 51160
661 GGGGATTAATACCGGCTTCCGGGTTTGTCAAGAGCTGTTATTGAAGAAACATCTAGAG 720

Db 51159 GGGATTATACACCGCTCCGGTTTCAGAGCTGTTATTGTAAGACATCTAGAG 51100
 Qy 721 CCGGGGCGCGATGAAACGAAAGGTGAAGCGCGCTTTCAATTTGGCAATATGACG 780
 Db 51099 CCGGGGCGCGATGAAACGAAAGGTGAAGCGCGCTTTCAATTTGGCAATATGACG 51040
 Qy 781 ATACCAAGGGCGCGATGAAACGAAAGGTGAAGCGCGCTTTCAATTTGGCAATATGACG 840
 Db 51039 ATACCAAGGGCGCGATGAAACGAAAGGTGAAGCGCGCTTTCAATTTGGCAATATGACG 50980
 Qy 841 GTGATGTGCAAGAACTGGAACCTGATGTTGAGCGCTTAAAGTGTTCGCGTAA 900
 Db 50979 GTGATGTGCAAGAACTGGAACCTGATGTTGAGCGCTTAAAGTGTTCGCGTAA 50920
 Qy 901 AAAGTAAATTTTTCATGAAAGCTGATGTTGAGCGCTTAAAGTGTTCGCGTAA 960
 Db 50919 AAAGTAAATTTTTCATGAAAGCTGATGTTGAGCGCTTAAAGTGTTCGCGTAA 50860
 Qy 961 GCAGAGAGAGTATTCATGAGCTTAATTA 990
 Db 50859 GCAGAGAGAGTATTCATGAGCTTAATTA 50830

RESULT 4 AE017333 40/c WPCOMMENT

Sequence split into 43 fragments LOCUS AE017333 Accession AE017333

Fragment Name	Begin	End
AE017333-00	1	110000
AE017333-01	100001	210000
AE017333-02	200001	310000
AE017333-03	300001	410000
AE017333-04	400001	510000
AE017333-05	500001	610000
AE017333-06	600001	710000
AE017333-07	700001	810000
AE017333-08	800001	910000
AE017333-09	900001	1010000
AE017333-10	1000001	1110000
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AE017333-30	3000001	3110000
AE017333-31	3100001	3210000
AE017333-32	3200001	3310000
AE017333-33	3300001	3410000
AE017333-34	3400001	3510000
AE017333-35	3500001	3610000
AE017333-36	3600001	3710000
AE017333-37	3700001	3810000
AE017333-38	3800001	3910000
AE017333-39	3900001	4010000
AE017333-40	4000001	4110000
AE017333-41	4100001	4210000
AE017333-42	4200001	4222645

Continuation (41 of 43) of AE017333 from base 4000001 (AE017333 Bacillus licheniformis D

Query Match 44.2%; Score 440; DB 1; Length 110000;
 Best Local Similarity 65.2%; Pred. No. 2.4e-108;
 Matches 647; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

Qy 4	ATGTCACAAATCTTACCTTGAAGAACTGCGTAAACAGTATTAAGCAAGAACATG 63
Db 52713	ATGTCACAAATCTTACCTTGAAGAACTGCGTAAACAGTATTAAGCAAGAACATG 52654
Qy 64	GATTTGCAATTTGAGCTTGAAGAACTGCGTAAACAGTATTAAGCAAGAACATG 123
Db 52653	GATTTGCAATTTGAGCTTGAAGAACTGCGTAAACAGTATTAAGCAAGAACATG 52594
Qy 124	AGTGAAGCTGACGGAAGGCCCATCAGACAGTACGCTTTATTCGTTATGCGGGA 183
Db 52593	AGTGAAGCTGACGGAAGGCCCATCAGACAGTACGCTTTATTCGTTATGCGGGA 52534
Qy 184	CTTGAATATATTTATTTGCGGACCGCATTTAATGAAGACGGTTATCTTTGCGGCT 243
Db 52533	CTTGAATATATTTATTTGCGGACCGCATTTAATGAAGACGGTTATCTTTGCGGCT 52474
Qy 244	TATTTCCGGGCTATGCGGATGACGAAACGATACCGGAAGATCCGTTCAATGTGC 303
Db 52473	TATTTCCGGGCTATGCGGATGACGAAACGATACCGGAAGATCCGTTCAATGTGC 52414
Qy 304	CCGCAATGATTTGACATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
Db 52413	CCGCAATGATTTGACATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 52354
Qy 364	AAAGTCAATCTTTACCATTTGTAAGAAATTAATTAATTAATTAATTAATTAATTA 423
Db 52353	GGGCTGTTTCTTTAAATGTTGTAAGAAATTAATTAATTAATTAATTAATTAATTA 52294
Qy 424	CTTCACTGATTTGCTGACGCGGCGGCGGAACTGACGATGAACCAAGACAGAC 483
Db 52293	CTTCACTGATTTGCTGACGCGGCGGCGGAACTGACGATGAACCAAGACAGAC 52234
Qy 484	GGGCTCAAGTCTATGATATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
Db 52233	GGGCTCAAGTCTATGATATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 52174
Qy 544	CATGTAACCAATCTGACGAAATTAACGAAATCAACGGAACCAATTAAGACAGAC 603
Db 52173	CATGTAACCAATCTGACGAAATTAACGAAATCAACGGAACCAATTAAGACAGAC 52114
Qy 604	ATGGCGGATTAAGCCCTTCTGCTTTGCGCAAGCTTAAGAACTGTTGCTGCGGCG 663
Db 52113	ATGGCGGATTAAGCCCTTCTGCTTTGCGCAAGCTTAAGAACTGTTGCTGCGGCG 52054
Qy 664	GATTAATACCGGCTTCCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Db 52053	GATTAATACCGGCTTCCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 51994
Qy 724	GGGCGCGATGAACGAAAGGTGTAACGCGCTTTTCAATTTGGCAATATGACGATA 783
Db 51993	GGGCGCGATGAACGAAAGGTGTAACGCGCTTTTCAATTTGGCAATATGACGATA 51934
Qy 784	CCAAAGGGCGCGATGAACGAAAGGTGTAACGCGCTTTTCAATTTGGCAATATGACG 843
Db 51933	CCAAAGGGCGCGATGAACGAAAGGTGTAACGCGCTTTTCAATTTGGCAATATGACG 51874
Qy 844	ATGTGCAACGAACTGGAATCTAATTTTCCACCACTATGACAAATGCGAAATCCAAAA 903
Db 51873	ATGTGCAACGAACTGGAATCTAATTTTCCACCACTATGACAAATGCGAAATCCAAAA 51814
Qy 904	GTAATTTTATTTCAATGAAGACCTGATGCTTTGAGGCTTAAGTGTTCCTGTAAGCA 963
Db 51813	GTAATTTTATTTCAATGAAGACCTGATGCTTTGAGGCTTAAGTGTTCCTGTAAGCA 51754
Qy 964	GAAGAGATTTATGAGCTTAATTAAGATC 995
Db 51753	GAAGAGATTTATGAGCTTAATTAAGATC 51722

RESULT 5
CP000002_40/c
WPCOMMENT

Sequence split into 43 fragments LOCUS CP000002 Accession CP000002

Fragment Name	Begin	End
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CP000002_02	200001	310000
CP000002_03	300001	410000
CP000002_04	400001	510000
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CP000002_37	3700001	3810000
CP000002_38	3800001	3910000
CP000002_39	3900001	4010000
CP000002_40	4000001	4110000
CP000002_41	4100001	4210000
CP000002_42	4200001	4222334

Continuation (41 of 43) of CP000002 from base 4000001 (CP000002 Bacillus licheniformis A

Query Match 44.2%; Score 440; DB 1; Length 110000;
Best Local Similarity 65.2%; Pred. No. 2.4e-108;
Matches 647; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

QY	4	ATGTGACAAAGTCTTACATTTGAAATCTGCTGACCGCTTAACATGATTTAGCAAGAACATG 63
DB	52599	ATGTGTACAAAGTCTTACATTTGAAATCTGCTGACCGCTTATTTAGCGAGACGATG 52540
QY	64	GATTTGCAATTTAGCTGGGAGACAGAGGTATTTCTATCGGCGCGTTACAGCTGAAC 123
DB	52539	GATTTGATTTTAAAGCTTAAACGGGAGAGTCTGTTGATCGGCTGCTAACAAATGAAA 52480
QY	124	AGTGAAGCTGACGGAAGGGCCATCAGACACAGTACGCGTTATTCGGTATGGGAGAAAA 183
DB	52479	AGTGAAGCGGACGCGACGACATGCGCGCTATGCGTTATTCGGATGGGACAAAG 52420
QY	184	CTTGAAGAAATATATTTATTTGCGGACGCGATTAAGAAAGCGTTATCTTGCGCGCTT 243
DB	52419	CTCAAGAAATGCTCTGTTGCGGATGCTGTAATGAAAGAGATGTTCTTGCGCGCGCTT 52360
QY	244	TATTTCCGGGCTATGCGGAGTACGAAAAAGATACGGGAGATACCGTTACATTTGTC 303
DB	52359	TATTTCCGGGCTATGCTGTTATGAAACGAAAGACAAAGCGGCAATCTTGCG 52300

QY	304	CCGCATGATTTGATGACATGGGTGCTGTCACTGCTGTCACTCTTTGGAAGACGTAAAGAA 363
DB	52299	CCGAGCAATTCGTGACATGGGTGCTGTCCGAAATGCGGCATTTGGAGATGTAAAGAA 52240
QY	364	AAATTCGATCTTTAAGATTTGAGAGAAAAATTAATCTATTTAGATTAACATTTTACCG 423
DB	52239	GGCGCTGTTCTTTAAACATTTGAGAGAGAGTCACTGCTGAGTACGATGACCGCG 52180
QY	424	CTTACATGATTTATTTGACACCGGAGCGGCAAACTGACATGAAACCAAGACGAC 483
DB	52179	CTGATTTGCTATTTAAGACCGCTCGGGCAAGCGTCTGTTGAAACCGACGAC 52120
QY	484	GGCTCAAGTCTATGATTAATCAACCTGCTGATGACGACACCGCCGATTTATATG 543
DB	52119	GGATTCATATTCATGATTAATCCGGTCCGCTGCTGACGACAGTCCGATTTCCCTGG 52060
QY	544	CATGTACCAATCTGACAGCAATTAACAGAAATCAGACCGAAGCAATTTAGACAAAG 603
DB	52059	CATTTGACCAATTTGGCAACTTTATCGTCTTCAACCGGACAGTTTCCGCAAAAA 52000
QY	604	ATGGGGAGTTAGCCCTTCTGCTTTTGCGCAAGGCTTAGAATGTTGCTCGCGG 663
DB	51999	ATGGAGGCTGACGCTGCTGCTTTGTCAGAGTTCCGGCTGTCGGATTCAGGA 51940
QY	664	GATTAATACCGGCTTCCGCTTGTGACAGCTGTTATTTGAAAGACATCTAGACCG 723
DB	51939	GATTTACGCGGCAATCCGCTTGTGACAGGCTGCAATTTTGAAGACATGAAAGCT 51880
QY	724	GCGGCGATGAAGCAAGAGGTGTAACAGCGCTTTCAATTTTGCAATATGACGATA 783
DB	51879	GTGTCCGATGAACCAAGAGCGCTGCGCGCTTCAATGCTCTCAATATGAAATAT 51820
QY	784	CCAAAGGGGCACTGATTAACGAGAAAGCAAAATCATTAATGCAATATCTTCGCTG 843
DB	51819	CTTAAAGGGGTGTATGACTGATCAAGGGCAAGACATTAACCAATATAGCGGTA 51760
QY	844	ATGTGACAAAGTCTGAAATCTATTTTCAACCACTATGACAAATCGCAATCAAAAA 903
DB	51759	ATGTGACGAGACGTCGACGCTATTTTCAACCAATTAACAAAGCAATTCAAAAAG 51700
QY	904	GTAATTTATTTTATGAAAGCTTGAAGCTTTGAGCCTTAAAGTTTCCGCTAAAGCA 963
DB	51699	GTTTCTTATTAAGAGAACCTGACACCAACCAATTAAGCGTTTCAGCCAAAGCAG 51640
QY	964	GAAAGAGTATTCATAGCTTAATTAAGATC 995
DB	51639	GAAAGACGCTTCAATTTCTTCAATCATTAAC 51608

RESULT 6
AX433304 990 bp DNA linear PAT 28-JUN-2002
LOCUS AX433304
DEFINITION Sequence 1719 from Patent WO0229113.
ACCESSION AX433304
VERSION AX433304.1 GI:21658108
KEYWORDS
SOURCE
ORGANISM Bacillus licheniformis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE
1 Berka, R. and Clausen, I. G.
METHODS for monitoring multiple gene expression
Patent: WO 0229113-A 1719 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S (DK)

FEATURES
source
1..990
/organism="Bacillus licheniformis"
/mol_type="unassigned DNA"
/db_xref="taxon:1402"

ORIGIN

Query Match 44.2%; Score 439.8; DB 6; Length 990;

Best Local Similarity 65.3%; Pred. No. 2.9e-108;
Matches 645; Conservative 0; Mismatches 342; Indels 0; Gaps 0;

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QY 4 ATGTGCAAGCTTCTTACATTGGAACCTGTGACCGTAAACATGTTATGCAAGAACATG 63
Db 1 ATGTGTACAAAGATACAGTTGACAGCTGGGCGCGAGCATTTATGCGGAGACGATG 60
QY 64 GATTTTGCACTTACAGTGGGAGACAGAGTATCTCTATCCGCGCGCTTACAGCTGAGAC 123
Db 61 GATTTTGATTTTGAAGCTTACCGGAGAGTGTCTGTGCAATCCGCGCTGCTACAAATGAAA 120
QY 124 AGTGAAGCTGACGGAAGGCGCCATCAACACAGTACGCTTTATGCTATGCGGAGAAA 183
Db 121 AGTGAAGCGGACGCGACGACGATCGCGCGCTATGCGTTATGCGGATGCGGAGAAA 180
QY 184 CTGGAATATATTTATTTGCGGACGCAATTAAGAAAGGCTTTATCTTGGCGGCGCT 243
Db 181 CTCAAGATGCTCTGTTTGGCCGATGCTGTAAGAAAAGATGCTTTGCGCGCGCTT 240
QY 244 TATTTTCCGGGCTATGCGGAGTACGAAAACGATPACGGGAGATACGCTTACATTTGTC 303
Db 241 TATTTTCCGGGCTATGCTGTGTATGAAAAGCAAGCAAAAGCAAGCGCAATCTTGGC 300
QY 304 CCGCATGAGTTTGTGACATGAGTGTGTGATCTGTCACTCTTTGAGACGTAAGAA 363
Db 301 CCGCATGAGTTTGTGACATGAGTGTGTGATGCGGATGCGGATTTGAGAGATGAAA 360
QY 364 AAGATTCGATCTTTAAAGATTTAGAGAAAATTTAGATCTATGATACATTTTACCG 423
Db 361 GCGGCTGTTTCTTAAACATTTGTGAGAGAGTCAAGCTTCTGATGAGTACGCGCG 420
QY 424 CTTCATGGAATATTTGACAGCGGAGCGGCGGAACTTACAGATAGAAACCAAGACAGAC 483
Db 421 CTGCAATGCTTATTAACGAGCGGCTCGGCGGAGAGTGTGTTGAACCGACGAGAC 480
QY 484 GGCCTCAAGTCTATGATATCAACCTGTGTGATGACGACGCCCGCATTTATATG 543
Db 481 GGCATTTCAAAATTCATGATATCCGCTGCGGTGCTGACCAAGCTCGGATTTCCCTTGG 540
QY 544 CATGTACCAATCTGACGACATATACAGAAATCAAGCCAGCAATTAAGAGCAAGAG 603
Db 541 CATTTGACCAATTTGGCACTTATCGGCTTTCAGCGCGGAGAGTTCCCGGAAAAA 600
QY 604 ATGGGCGGATTAAGCCCTTTCTGCTTTGGCAAGGCTTAGAACTGTGTGCGCGGG 663
Db 601 ATGGGAGGCTTACGCTGTGCGCTTTTGTCAAGGTTCCGCGCTGCCGATTTGCCAGA 660
QY 664 GATTAATACACGCGCTTCCGCGTTTGTCAAGCTGTTTATTTGAAAGACATCTAGCGG 723
Db 661 GATTTTACCGCGCATCCGCTTGTCAAGGCTGCAATTTTGAAGACATGAGAGCT 720
QY 724 GCGGCGGATGAAAGCAAGGCTGTCAAGCGCTTTTCAATTTTGGCAATTAAGAGAA 783
Db 721 GGTGTCCGATGAAACAGAAAGCGCTCTGCGCGCTTTCATGCTCTCAATAGAAATTT 780
QY 784 CCAAGAGGCGAGTGAATTAACGGAAGAAAGCAATTAATCAAGCAATATCTTCCGTG 843
Db 781 CCAAGAGGCTTATGATGATGATCAAGGAGAAAGATTAATCAAGCAATATCGGGGGA 840
QY 844 ATGTGCAAGCAAGCTGGAACCTATATTTCCACCACTATGACATGCGCAATCCAAA 903
Db 841 ATGTGCAAGCAAGCTGGAACCTATATTTCCACCACTATCAAAAGCAAGATTTCAA 900
QY 904 GTTAATTTTATTTATGAGAGCTTGAAGCTTTGAGAGCTTAAAGTTTCCGTAAAGCA 963
Db 901 GTTTGCTTTTATGAGAGAGCTTGAAGAGCTTGAAGAGCTTTTCCGCAAGAGCA 960
QY 964 GAAGAGATATTCATGAGCTTAAATTA 990
Db 961 GAAGAGAGCTTATCTCTTCAATCA 987

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RESULT 7

AE017225.35/c
WPCOMMENT
Sequence split into 53 fragments LOCUS AE017225 Accession AE017225

Fragment Name	Begin	End
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AE017225_02	200001	310000
AE017225_03	300001	410000
AE017225_04	400001	510000
AE017225_05	500001	610000
AE017225_06	600001	710000
AE017225_07	700001	810000
AE017225_08	800001	910000
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AE017225_42	4200001	4310000
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AE017225_47	4700001	4810000
AE017225_48	4800001	4910000
AE017225_49	4900001	5010000
AE017225_50	5000001	5110000
AE017225_51	5100001	5210000
AE017225_52	5200001	5228663

Continuation (36 of 53) of AE017225 from base 3500001 (AE017225 Bacillus anthracis str

Query Match 29.4%; Score 293.2; DB 1; Length 110000;
Best Local Similarity 55.9%; Pred. No. 1.9e-68;
Matches 556; Conservative 0; Mismatches 438; Indels 0; Gaps 0;

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QY 3 TATGTCAAGCTTCTTACATTGGAACCTGTGACCGTAAACATGTTATGCAAGAACAT 62
Db 71198 TATGTGTACTTATGATTTGACATTTAGACCAAAAACGCTACGATCTTTTGGCAAGACAT 71139
QY 63 GGAATTTGCACTTACAGCTGGGAGACAGAGTGAATTTCTATCCGCGCGTTACAGCTGGA 122
Db 71138 GGAATTTGCACTTATGATATGATCAAGAGTAAATTAATCAATTTCTTCAATTAACAGTGA 71079
QY 123 CAGTGAAGCTGACGGAAGGCGCCATCAGACAGATGAGGCTTATCGGTATGCGGAGAA 182

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Dp	71078	AAATATTAACGGSGTAATCATTAAATAGAAACATGCTACGGTGGCAATGGGTATTAATCA	71012
Qy	183	ACTTGGAAATATATTATTATTGCGCACGGCATTATGAAGAAGCGGTTATCTTGTGCGGCGCT	242
Dp	71018	TCAMGGAAAGGATTCATTATATGCGCGACCGGAGTAAATGAAGCAGGTATGATCATGTGCAACACT	70958
Qy	243	TTATTTTCCGGGCTATGCGGAGTACGAAAAAAGCATACGGGAAGATACCGTTACATTTGT	302
Dp	70958	CTATTTTCCAGATATCGCTACTTATATGCAACAGATATGATGACACAAACGAATTTGCG	70899
Qy	303	CCCGCATGATTTTGACATGSGGTGTCTCAGTCTGTCAGTCTTTTGAAACCTTAAGA	362
Dp	70898	TCCATTTGATTTTGAACTTGAGCTGACACAATTCATTCGTGTAAGAAGTTAAAGA	70839
Qy	363	AAAGATTCGATCTTTAAGATTGTGAGAAAAAATTGATCTATGTGATCAAGTTTACC	422
Dp	70838	ATCTGTGATATGCAATACCTTTTGGATATACATTCACCGAATTTTGGACTTACCGCACCC	70779
Qy	423	GCTTCACGTGATATTTGTGACACCGGACGGGCGGAACTTGACATATGAACCAAGACAGA	482
Dp	70778	ACTACATTTGATTTTATGCGGATAAATGGGAGATGTGATTTGTACTGATCCGACAGTGA	70719
Qy	483	CGGCTCAGAGTCTATGATTAATCAACTGTGTGTCAGACGACACGCCGACTTTATATG	542
Dp	70718	AGGATTTAAATTTGTATGATTAACCACTACGAGGTGATGACAAATATGCTCCGAGTTTATG	70659
Qy	543	GCATGTACCAATCTGCGAGCAATATACAGGAATACGACGAGACATTTAGAGGCAAGA	602
Dp	70658	GCATTTACAAATTTTAAAGACATATATATAGGCTTTAAATCCGACCATTTGCGCCACAGA	70599
Qy	603	GATGCGCGGATTAAGCCCTTCTGCTTTTGCCCAAGGCTTATGAACTGTGTGCTGCGG	662
Dp	70598	GTGAGATTAATTTACATTAAGTGTCTTTTGCCCAAGGCTCGGGCTCAATGGGACTTCAG	70539
Qy	663	GGATTTATACACCGGCTTCCGSGTTGTGCAGAGCTTTATTTAAAGAACATCTAGGCC	722
Dp	70538	GGATTTCACTCCCGCATCTGAGGTTTGTGCGGCGACGATATGSCAAACAAACATTCAG	70479
Qy	723	GGCGCGCATGAAACGAAAGGTGTAAACGCGCGCTTTTCAAAATTTTGCCAAATATGCAAT	782
Dp	70478	TATAGATATGCGAAGAGAGGGAAGTATCAGCCCTTTTCAATCTTATCAAAATTTGAGAGT	70419
Qy	783	ACGAAAGGCGGCACTGTAACGAAAGAAAGCAAAATTCATTATAGCAATATATCTTCGT	842
Dp	70418	TCCTTAAAGGTGAGATTAATACAGAAAGGTGCAATTGATTAATATCATATATACAGCGT	70359
Qy	843	GATGTGCAAGAACTGGAACCTACTTTTCCAACCTATGACAAATCGGCAATCCAAA	902
Dp	70358	AATGTGTATGGAATCCGGAACATATATTTATCATCTTACGATTTGTAGACAAATTTATAC	70299
Qy	903	AGTAAATTTATTTCATGAAAGCTTGACTGTTTGGAGCCCTAAAGTGTTTTCGCTAAAGC	962
Dp	70298	TGTTCACTTTATTTTCATGAAATTTAGATACAGATGAGATTAAAGCTATCCGTTCAAG	70239
Qy	963	AGAGAGAGATTCATGAGCTTAATTAAGATCC	996
Dp	70238	GAACCAAAAATATTTATATGAACTATGATAGCC	70205

Fragment Name	Begin	End	Sequence split into 53 fragments	LOCUS	AE017334	Accession	AE017334
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AE017334_06	60001	71000					
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AE017334_08	80001	91000					

AE017334_09	900001	110000
AE017334_10	1000001	111000
AE017334_11	1100001	121000
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Continuation (36 of 53) of AE017334 From base 3500001 (AE017334 Bacillus anthracis str.

Query Match	29.4%	Score 293.2	DB 1	Length 110000
Best Local Similarity	55.9%	Pred. No. 1.9e-68		
Matches 556	Conservative 0	Mismatch 438	Indels 0	Gaps 0
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 ACCESSION AEO17036
 VERSION AEO17036.1 GI:30258352
 KEYWORDS
 SOURCE
 ORGANISM
 Bacillus anthracis str. Ames
 Bacillus anthracis str. Ames
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
 1 (bases 1 to 291030)
 Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,
 Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzaple, E.,
 Oksstad, O., Helgason, E., Ristone, J., Wu, M., Kolonay, J., Beaman, M.,
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 Berry, K., Plant, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,
 Cline, R., Redmond, C., Thwaite, J., White, O., Salzberg, S.,
 Thompson, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
 Fraser, C.
 The genome sequence of Bacillus anthracis Ames and comparison to
 closely related bacteria
 JOURNAL
 Nature 423 (6935), 81-86 (2003)
 PUBMED
 12721629

REFERENCE 2 (bases 1 to 291030)
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 source
 gene
 CDS
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Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,
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 Direct Submission
 Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
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QY 783 ACCAAGGCGGATGATTAAGCAAGAGCAAAATCTATATAGCAATATCTCCGT 842
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DB 60842 AATGTATGGAATCCGGAACATATATATCATCTTACATGATGAGCAATATATAGC 60783
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AE017355_10	1000001	1110000
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continuation (36 of 53) of AE017355 from base 3500001 (AE017355 Bacillus thuringiensis)

Query Match 29.2%; Score 290.6; DB 1; Length 110000;
Best Local Similarity 55.8%; Freq. No. 9.7e-68;
Matches 554; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

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DB 96518 GGAATTCACATTAAGTATGATTAAGTATGAGTATATATATCTTCTCGACATTAAGTGA 96459
QY 123 CAGTGAAGCTGACGAGAGGCGCCATCAGACAGTACCGCTTATCGGTATGCGGAGAA 182
DB 96458 TAAATTAACCGGATGAATCAATTAATGAGAACTGCTAGCGGTGAATGGAAATTAATCA 96399
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DB 96398 TCAAGAGAGATCATTAATGCGGACGAGTAAATGAGCAGATGATGCGCAACT 96339
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RESULT 11
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ACCESSION AE017001 AE016877
VERSION   AE017001.1 GI:29894619
KEYWORDS SOURCE
ORGANISM Bacillus cereus ATCC 14579
           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
REFERENCE 1 (bases 1 to 304708)
AUTHORS Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelson,B.,
           Kapratel,V., Bhattacharya,A., Resnik,G., Mikhailova,N.,
           Lapidus,A., Chu,L., Mazur,M., Goldsman,E., Larsen,N., D'Souza,M.,
           Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
           Ehlich,D.S.D., Overbeek,R. and Kyrpides,N.
           Genome sequence of Bacillus cereus and comparative analysis with
           Bacillus anthracis
           Nature 423 (6935), 87-91 (2003)
JOURNAL  1271630
PUBMED   2 (bases 1 to 304708)
AUTHORS Candelson,B., Galloux,K., Ehrlich,D.S. and Sorokin,A.
TITLE    The number of ribosomal RNA operons in Bacillus cereus
JOURNAL  Unpublished
REFERENCE 3 (bases 1 to 304708)
AUTHORS Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelson,B.,
           Kapratel,V., Bhattacharya,A., Resnik,G., Mikhailova,N.,
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           Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
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           Direct Submission
           Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de
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AUTHORS	Glaser, P., Fraungaul, L., Buchrieser, C., Ruhnok, C., Amend, A., Baquero, F., Berche, P., Bloecher, H., Brand, P., Chakraborty, T., Charbit, A., Cheroutani, F., Couve, B., De Daruvar, A., Denoux, P., Domant, E., Dominguez-Bernal, G., Duchaud, S., Durant, L.,				

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 Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and
 Coesart, P.
 Comparative genomics of *Listeria species*
 Science 294 (5543), 849-852 (2001).
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 Glaeser, P., Frangeul, L. and Rusniok, C.
 Direct Submission
 Submitted (06-JUN-2001) Glaeser P., Institut Pasteur, Genomique des
 Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
 Cedex 15, FRANCE
 E-mail: pglaser@pasteur.fr
 Phone: +33 1 45 68 89 96, Fax: +33 (0) 1 45 68 87 86.
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119620 TGTATCTTGTTCGAGAGAGATTAAGAAAATATGA 119655

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RESULT 14

AX641665 349980 bp DNA linear PAT 21-FEB-2003
 LOCUS
 DEFINITION Sequence 2855 from Patent WO0101118.
 ACCESSION AX641665
 VERSION AX641665.1 GI:28474426
 KEYWORDS
 SOURCE
 ORGANISM
 Listeria monocytogenes
 Listeria monocytogenes
 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1 Buchrieser, C., Frangeul, L., Couve, E., Ruanlok, C., Fsihi, H.,
 Deloux, P., Dissergue, O., Chetoui, F., Nedjati, H., Glaser, P.,
 Kunet, F., Cosset, P., Danile, J., Goebel, W., Kieft, J., Kuhn, M.,
 Ng, E., Vazquez-Boland, J., Dominguez-Bernal, G., Garrido-Garcia, P.,
 Trierer-Martinez, A., Amend, A., Chakraborty, T., Domann, E., Hain, T.,
 Berche, P., Charbit, A., Durant, L., Perez-Diaz, J. C., Baquero, F.,
 Garcia del Portillo, F., Gomez-Lopez, N., Madueno, E., de Pablos, B.,
 Wehland, J., Kaerz, D., Entian, K. D., Haut, J., Rose, M., and Voss, H.
 Listeria monocytogenes genome, polypeptides and uses
 JOURNAL
 PATENT: WO 0101118-A 2855 11-APR-2001;
 INSTITUTE PASTEUR (FR)

FEATURES

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 1..349980
 location/Qualifiers
 /organism="Listeria monocytogenes"
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 to 0.649.980 length: 349.980 <223>-seq 2856 : From
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GenCore version 5.1.7
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(without alignments)

10212.360 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 9993994

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Maximum Match 100%

Listing first 45 summaries

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11: geneseq2003ds.*
12: geneseq2004as.*
13: geneseq2004bs.*
14: geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	996	14 AEA39623	Aea39623 Bacillus
2	439.8	44.2	990	6 ABK74428	Abk74428 Bacillus
3	287.8	28.9	984	8 ACA21250	ACA21250 Prokaryot
4	237	23.8	969	6 ACA21947	ACA21947 Prokaryot
5	233.6	23.5	110000	6 ABA03041_04	Continuation (5 of
6	232.6	23.4	990	6 ABO69869	Abog69869 Listeria
7	232.6	23.4	990	6 ABO67953	Abog67953 Listeria
8	232.6	23.4	990	6 ACA36885	ACA36885 Prokaryot
9	196.4	19.7	1087	13 ADR89833	ADR89833 Clostridi
10	177	17.8	110000	6 ABA90521_18	Continuation (19 o
11	177	17.8	110000	6 ABA90521_19	Continuation (20 o
12	173.8	17.4	1616	12 ACPE57607	ACPE57607 B sphaeri
13	173.8	17.4	1616	12 ADG62865	ADG62865 B sphaeri
14	160.2	16.1	978	8 ACA46430	ACA46430 Prokaryot
15	159	16.0	990	4 AAH52510	AAH52510 S. epider
16	159	16.0	996	6 ABA92958	ABA92958 Staphyloc
17	159	16.0	996	13 ADO502160	ADO502160 Staphyloc
18	159	16.0	2975	4 AAH53981	AAH53981 S. epider
19	159	16.0	4114	4 AAH54820	AAH54820 S. epider

20	146	14.7	993	8 ACA20090	ACA20090 Prokaryot
21	146	14.7	999	8 ACFF73532	ACFF73532 Staphyloc
22	142.8	14.3	1002	4 AAH54746	AAH54746 Staphyloc
23	142.4	14.3	981	4 AAH52083	AAH52083 Staphyloc
24	127.6	12.8	11466	2 AAH74755	AAH74755 Staphyloc
25	117.8	11.8	972	8 ACA47889	ACA47889 Prokaryot
26	106.8	10.7	110000	10 ADF77343_00	ADF77343 Lactic ac
27	104	10.4	4027	13 ADR89831	ADR89831 Lactobact
28	104	10.4	110000	10 ADF77343_14	Continuation (15 o
29	97.6	9.8	975	13 ADR89827	ADR89827 Lactobact
30	96	9.6	975	2 AAQ38722	AAQ38722 BSH gene
31	95.4	9.6	972	8 ACA33036	ACA33036 Prokaryot
32	95.4	9.6	987	10 ADH82953	ADH82953 Enterococ
33	82.6	8.3	978	10 ADC90739	ADC90739 E. faeciu
34	80.6	8.1	972	8 ACA33846	ACA33846 Prokaryot
35	80.2	8.1	349980	6 ABO81846	ABO81846 Bifidobac
36	79.4	8.0	110000	10 ADF77343_12	Continuation (13 o
37	79.2	8.0	954	4 AAF89390	AAF89390 Bifidobac
38	72.4	7.3	1050	8 ACA24329	ACA24329 Prokaryot
39	63.6	6.4	978	6 ABO70013	ABO70013 Listeria
40	63.6	6.4	978	6 ABO68098	ABO68098 Listeria
41	63.6	6.4	110000	6 ABA03041_21	Continuation (22 o
42	62.2	6.2	2000	8 ADA71938	ADA71938 Rice gene
43	61.8	6.2	579	8 ACA33669	ACA33669 Prokaryot
44	55.2	5.5	1092	8 ACA52200	ACA52200 Prokaryot
45	54.8	5.5	4118	12 ADO32293	ADO32293 Bacterial

ALIGNMENTS

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ID	AEA39623	
AC	AEA39623;	
XX		
DT	08-SEP-2005 (fixet entry)	
XX		
DE	Bacillus subtilis conjugated bile acid hydrolase gene, SEQ ID NO.1.	
KW	Plasmid, conjugated bile acid hydrolase; penicillin V acylase;	
KM	choleylglycine hydrolase; penicillin amldase; gene; ds.	
XX		
OS	Bacillus subtilis; NCIMB 11621.	
XX		
PH	Key	Location/Qualifiers
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FT		/product= "Conjugated bile acid hydrolase gene"
FT		/EC number= "3.5.1.24"
FT		/note= "Has penicillin V acylase (EC 3.5.1.11) activity"
XX		
PN	US2005142652-A1.	
XX		
PD	30-JUN-2005.	
XX		
XX	30-MAR-2004; 2004US-00812387.	
PF		
XX		
PR	24-DEC-2003; 2003WO-IB006198.	
XX		
PA	(COUL) COUNCIL SCI & IND RES SOUTH AFRICA.	
XX	(UYUO-) UNIV YORK.	
PI	Sivranan H, Pundle AV, Sureeh CG, Dodson GG, Brannigan JA;	
XX		
DR	WPI; 2005-457790/46.	
XX		
PT	New recombinant plasmid containing a chromosomal DNA fragment from	
PT	Bacillus subtilis encoding conjugated bile acid hydrolase, useful for	
PT	producing large amounts of penicillin V acylase.	
XX		
PS	Claim 1; SEQ ID NO 1; epp; English.	

CC gene, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which *Bacillus* cells adapt to changes in culture conditions.
 CC environmental stress or other physiological provocation. Extensive follow
 CC up characterization is unnecessary, when one spot on an array equals one
 CC gene or one open reading frame, since sequence information is available.
 CC This sequence represents a genomic sequence tag (GST) used in the method
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 990 BP, 247 A, 214 C, 285 G, 244 T, 0 U, 0 Other;

Query Match 44.2%; Score 439.8; DB 6; Length 990;
 Best Local Similarity 65.3%; Pred. No. 3,1e-129;
 Matches 645; Conservative 0; Mismatches 342; Indels 0; Gaps 0;

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DB 1 ATGTGTAAGATGATCACTGTGACGCGCGGAGCATTTATGCGAGAGCAATG 60
QY 64 GATTTGCAATTCAGTGGGAGCAGAGGTGATCTATCCGGCCGTTACAGCTGGAAC 123
DB 61 GATTTGATTTTGAAGCTTAAACGGGAGGAGTCTTGTGATCCGCTGCTCAAAATGAAA 120
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DB 541 CATTTGACCAATTTGGGCAACTTTATCGGCTTTCACCGGACAGATTTCCGGAGAAAAA 600
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RESULT 3
 ACA21250
 ID ACA21250 standard, DNA; 984 BP.

ACA21250;
 19-JUN-2003 (first entry)

Prokaryotic essential gene #2907.

Antisense; ds; prokaryotic essential gene; cell proliferation;
 drug design; gene.

Bacillus anthracis.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002MO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen K, Zykkind JW,
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

P-PSDB; AB017380.

New antisense nucleic acids, useful for identifying proteins or screening
 for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 9120; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of
 the 623 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-required gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism acts; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 984 BP; 336 A; 165 C; 207 G; 276 T; 0 U; 0 Other;

Query Match 28.9%; Score 287.8; DB 8; Length 984;

Best Local Similarity 56.0%; Pred. No. 1.1e-80; Matches 544; Conservative 0; Mismatches 427; Indels 0; Gaps 0;

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DB 1 ATGTGTACTAGTTGACATTAGACAAACAAACGGTCAGCATCTTTTGCAGAACGATG 60
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QY 184 CTGGAATATTTATTTTCCGACGAGGATTAATGAAGGCTTTATCTTTCGCGGCTT 243
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QY 244 TATTTTCGCGGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
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DB 301 CCATTTGATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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QY 424 CTTCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
DB 421 CTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 484 GGCCTCAAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
DB 481 GGATTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 544 CATGTACCAATCTGAGCATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 603
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QY 604 ATGGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 663
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DB 661 GATTTACACCGCTTCCGCTTGTGACAGCTGTTTATTTGAAAGACATCTAGAGCT 720
QY 724 GGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
DB 721 ATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 784 CCNAGGCGGAGTGTATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843

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DB 781 CCTTAAAGTGAAGTAAATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
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DB 841 ATGTGTGAGATCCGGAACATTTATTAATCACTTACATTTGATGACAAATTAATGCT 900
QY 904 GTAAATTTATTTCAATGAAGCCTTGAAGCTTTGAGGCTTAAGTGTTCGCTAAAGCA 963
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DB 961 AAACAAAAAAT 971

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RESULT 4

ACA21947
ID ACA21947 standard; DNA; 969 BP.

ACA21947;

19-JUN-2003 (first entry)

DE Prokaryotic essential gene #3604.

KW Antisense; ds; prokaryotic essential gene; cell proliferation;

drug design; gene.

OS Bacillus anthracis.

PN WO20027183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.

XX P-PSDB; ABU18077.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 9817; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX cell proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)

XX identifying a gene required for cellular proliferation or the biological

XX pathway in which a proliferation-required gene or its gene product lies

XX or a gene on which the test compound that inhibits proliferation of an

QY	243	TTATTTTCCGGGCTATGGCGAGTACGAAAAACGATACGGAAAGATACGGTTCACATTTG	302
Db	78960	ATATCTTCACGGAGAAAGCATTTATGTGGCCAGACCACTGGAAAGAAAAATCAATTTAGC	79019
QY	303	CCCGCATGAGTTGTGCATGGGTCGTCACTCTCAGTCTTTTGGAGACGTAATAAGA	362
Db	79020	TCCACAAGAATTTTGTCTTTGGCTGTTAGAATTTCGCAACGATTAAGAATGTGAAC	79079
QY	363	AAAGATTCGATCTTTAACGATTGTAGAGAAAAAATTGATCTAATTGGATACAGTTTACC	422
Db	79080	AAAGTTATCGGTTATATACTTGTGGATCAACCAAGTACGGTTACTTGGATACAAACACC	79139
QY	423	GCTTCACTGATATTTGTCAACCGGACGGCCGAAACTGACGATAGAACAAAGACAGA	482
Db	79140	ATTACACTGGATTTTTCACAGCAAGAGTGGCCGTGTGTGTGATTTGAACCAACAGAAAC	79199
QY	483	CGGCTCAAGTCTATGATATATCAACCTGGTGTATGAGAAAGGCCCGCATTTATATG	542
Db	79200	ATCGCTTCGTATTAATAAAGAAACCTGTGAGAGTTATGACAAATAGCCACACGATCGAATG	79259
QY	543	GCAATGTAACCAATCTGCAGCAATATACAGAAATCAGACCGAAACAAATTAGAGACAAAGA	602
Db	79260	GCAATATGAGAAATTTACGACACTACACAGGTTTACAGCAACACAAATTTAGCCGCGTGA	79319
QY	603	GATGGCGGAGATTAGCCCTTCTGCTTTTGGCCAAAGCTTAGAACTTTGGTCTGCCGG	662
Db	79320	GTTTCGAGAGATATATGCGTAAACCATTTTCGCAAGGTACAGGAACAAAGAAATTAACAAG	79379
QY	663	GGATTAATACACCGGCTTCCGGTTTGTACAGCTGTTATTGTAAGAATCTTAAGCC	722
Db	79380	TGTTTAATCTCCGCGAGAAAGTTTTGTCCGTGGCGATACCTTAAGAAAAATTTATAAA	79439
QY	723	GGCGCGGATGAACGAAGGTGTAAACGCCGCTTTCAATTTTGGCAAAATATGACAT	782
Db	79440	AGCGAAAAACGAAGAAAGTATCACAAAATGTGTGTATGTCTTGAAACAGTCCGCAAT	79499
QY	783	ACCAAGGCGCGACATGATTAACGAAGAAGACGAATTCATTATACGATATATCTTCGAT	842
Db	79500	TCCGAATGAGACGGTAATTAAGAAAGTGGTGAACCTGATTTCAACAATATGTGGCATC	79559
QY	843	GATGTGCAAGAACTGGAAACTATCTATTTTCACACTATATGACATCGGCAATCCAAA	902
Db	79560	TATGTGTTCCGAAAGCAAAAGTACTCTTTTCACTCATACGAAACAAACCAATCATATG	79619
QY	903	AGTAATTTATTTCAAGAAAGCTGACTGTTTGA	938
Db	79620	TGTTACTTTGTCAAGAAAGTTATAGAAAATATATA	79655

RESULT 6	
ABQ69869	
ID	ABQ69869 standard; DNA; 990 BP.
XX	
AC	ABQ69869;
XX	
DT	29-AUG-2003 (revised)
DT	29-AUG-2002 (first entry)
XX	
DE	Listeria monocytogenes EGDe DNA sequence #81.
XX	
KM	Antibacterial; Listeria; food contamination; mutational analysis
KM	Infection; ds.
XX	
OS	Listeria monocytogenes; EGDe.
XX	
PN	WO200228891-A2.
PD	
XX	
PD	11-APR-2002.
XX	
PF	04-OCT-2001; 2001MO-FR003061.
PR	04-OCT-2000; 2000FR-00012697.

XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX
PI Kunst F, Glaser P;
XX
XX WPI: 2002-332479/37.
XX
XX New genomic sequences from *Listeria* species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators.
XX
XX Claim 16; SEQ ID NO 2682; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences (AB067188-
CC AB071212) from *Listeria* sp. The sequences are useful as probes and
CC primers for identification and/or detection of *Listeria* (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of gene
CC expression. Proteins encoded by the nucleic acid sequences can be used to
CC screen for compounds that modulate gene expression, replication and
CC pathogenicity of *Listeria* (potential therapeutic agents), also for
CC treating infections by *Listeria*, and are useful as immunogens in anti-
CC *Listeria* vaccines. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIFO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences). (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 990 BP; 347 A; 171 C; 215 G; 257 T; 0 U; 0 Other;

Query Match	Similarity	Score	DB 6	Length	990
Beet Local	53.0%	Pred. No. 4,7e-63			
Matches	Conservative	0	Mismatches	439	Indels
					Gaps
					0
Db					
4	ATGTGCACAAAGTCTTAACTTGAAGAACTGTGTAACGCTAAACATGTATTTAGCAAGAACATG	63			
1	ATGTGCACAAAGTCTTAACTTGAAGAACTGTATGAGAAACATTTATTTATTCAGAAACGATG	60			
64	GATTTTGCATTTCACTTGGGACAGAGGTGATTCCTATCCGCGCGGTTACAGCTGGAGC	123			
61	GATTTTGCCTTTATTTTGGAGGCGAACCCACATTTAGCCACAGAAATTTATGATGGAAA	120			
124	AGTGAAGCTGACGGAAAGGCCATCAGACAGAGTACGCGTTATCGTATGAGGAGAAA	183			
121	TCTTTCTACAGACGGTCCCATTTATTTATAGATATGCAATTTGTTGAGCGGGAGAGAG	180			
184	CTTGAATAATATTTATTTGCGCAGCGCATTTATGAAAGCGTTTATCTTGTGCGCGCTT	243			
181	TTAGATTAATACTTTTGGCAGACCGGATGTGATGAAAGGATTTAAGCTGTGCATCTTCA	240			
244	TATTTTCCGGGCTATGCGGAGTACGAAATAAAGATACGGGAAGATACCGTTCACTTGTG	303			
241	TATCTTCCAGGAGAACAGTTTATGCGCAGACACAGTGGAGGAAAAATCAATTTAGCT	300			
304	CCGCAATGATTTGTGACATGGGTGCTGTCAGTCTGTCACTTGTGGAAGACGTAAAGAA	363			
301	CCACAAGATTTTGTGCTTGGCTGTTAGGAACCTGCGCAACGATTAAGATGTGGAAGCA	360			
364	AAGATTCATCTTTAACCATTTTAAGAAAAAATTAGATCTATTTGATACATTTTATCCG	423			
361	AAGTTATCGGTATTAACCTTGTGTGATCAACAGTACCGCTTATCTTGGAAATCACACACCA	420			
424	CTTCACTGATATTGTGACAGACCGGACGGGCGGAACTTGACGATAGAACCAAGACGAGC	483			
421	TTACACTGATTTTACAGACCAAGAGTGGGCGTGTGTGATTTGAACCAACAGAAACA	480			
484	GGCTTCAAAGTCTATGATATCAACCTGTGTCTATGACGAACAGACCCCGCATTTATATGG	543			
481	TGCTTCGTATTAAGAAACCCTGTAGAGATTAAGCAAAATACGCAACGATCGAATGG	540			
544	CATGTAAACCAATCGACGAATATTCAGGAATCAGACCAAGCAATTAAGAGCAAGAG	603			
541	CATATGAGAAATTTAGCAACTACACAGGTTTACAGACCAACATTTAGCCCGCGTGAAG	600			

QY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTAGAAGTGTGGTCCCGGG 663
DB 601 TTGGAGAGTATATGCTTAAACATTTTCGAAAGTACAGGAACAGCAATTAACAGGT 660
QY 664 GATTATACACCGCTTCCGGTGTTCAGAGCTGTATTTGAAAGACATCTAGACCG 723
DB 661 GGTATATCTCGCGCAGAACGTTTTGTCCGTCCGSCATCTTGAAAGAAATATTTAAAA 720
QY 724 GCGCGCATGAAACGAAAGGTATACAGCCGCTTTCAAAATTTGGCAAAATATAGCATA 783
DB 721 GCGAAAAACGAAAGAGCTATCAAAATGTGTATGTCTTGAACAGTGTCCGATT 780
QY 784 CCAAGGGCGCAGATGAAGAGAGAGAAATTCATTAACGATATCTTCCTGT 843
DB 781 CCGAATGAGCGGTAATTAAGAAAGTGTGACCTGATTTACACAAATATGTGGCATCT 840
QY 844 ATGTGCAACGAACTGGAATCTATTTCCACACTATGACAAATCGCAAAATCCAAAA 903
DB 841 ATGTGTTGCGAAGGCAAAAGCTACTTTTCACTCATACGAAACAAATCAATAGT 900
QY 904 GTAAATTTATTTCATGAAAGCTTGAAGCTTTGGA 938
DB 901 GTTACTTTGTCAAGAGGATTAAGAAATATGAA 935

RESULT 7
AB067953
ID AB067953 standard; DNA; 990 BP.
XX AB067953;
AC 29-AUG-2003 (revised)
DT 29-AUG-2002 (first entry)
DE Listeria monocytogenes EGD DNA sequence #77.
XX Listeria monocytogenes EGD DNA sequence #77.
KM Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
OS Listeria monocytogenes; EGD.
XX MO200228891-A2.
XX 11-APR-2002.
PD 04-OCT-2001; 2001WO-FR003061.
XX 04-OCT-2001; 2001WO-FR003061.
PF 04-OCT-2000; 2000FR-00012697.
PR (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA Kunet F, Glaeser P;
XX WPI, 2002-332479/37.
DR New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
XX antibodies and modulators.
XX Claim 16; SEQ ID NO 766; 1800p; French.
XX The present invention relates to nucleic acid sequences (AB067188-
CC AB071212) from Listeria sp. The sequences are useful as probes and
CC primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of gene
CC expression. Proteins encoded by the nucleic acid sequences can be used to
CC screen for compounds that modulate gene expression, replication and
CC pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in anti-
CC Listeria vaccines. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated

CC on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 990 BP; 347 A; 171 C; 215 G; 257 T; 0 U; 0 Other;
Query Match 23 4%; Score 232.6; DB 6; Length 990;
Best Local Similarity 53.0%; Pred. No. 4,7e-63;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;
QY 4 ATGTGCAACAGTCTTACATTTGAAAGTGTGACCTGTAACATGATATAGCAAGACATG 63
DB 1 ATGTGCAACAGTCTTACATTTGAAAGTGTGACCTGTAACATGATATAGCAAGACATG 60
QY 64 GATTTCATTTGACGTGGAGACAGAGTGTCTTATCCGCGCGGTTACAGCTGAGAC 123
DB 61 GATTTCATTTGATTTTGGAGGGGCAACCAACATTAAGCCCAAGAAATATATGATGAAA 120
QY 124 AGTGAAGCTGAGGAGAGGGCCCATGACAGACAGTACGCTTTATGCGTATGGGAGAAAA 183
DB 121 TCTTCTACAGACGGTGCCAAATTAATTAATGATATGCAATTTGTGAGCGGGAAGAG 180
QY 184 CTGGAATATATATATTTATGCGCAGCATTAATGAAGCGGTTATCTGTGCGGCGCTT 243
DB 181 TTAGATATATATCATTTTCCAGACGGATTAATGAAGAGATTAAGCTGTGATCTCTA 240
QY 244 TATTTTCCGGGCTATGCGGAGTACGAAAAACGATACGGAGATACCGTTCAATGTC 303
DB 241 TATCTTCCAGAGAGAGCAGTTTATGCGCCAGACCAAGTGAAGAGAAAAATCAATTAAGCT 300
QY 304 CCGCATGATTTGTGACATGAGGTGCTGTCAAGTCTGTCACTCTTTGAAAGACGTAAGAA 363
DB 301 CCAACAAGAAATTTTGTGTTGGCTGTGAGAACCTTGCAACATTAAGATGTGAAGCA 360
QY 364 AAGATTCAGTCTTTAAAGATGTGAGAAATAATAGATCTATGTGATACAGTTTAAACG 423
DB 361 AAGTATCGGTTATTAACCTTGTGATGATCAACAGTACCGTTACTTGGAATCACAACCA 420
QY 424 CTTCACGTGATATGTGACAGCGGACGGCGGAAACCTGACATGAGAACCAAGACAGAC 483
DB 421 TTACACTGATTTTTCACAGACAGAGTGGCGCTGTGTGATGATGAACCAACAGAAACA 480
QY 484 GGCCTCAAGTCTATGATTAATCACTGCTGTCAATGACAGACCGCCGCACTTATATG 543
DB 481 TCGCTTCGTATTAAGAAACCTTGTGAGATTAAGCAAAATGCGCAGCATGAGATG 540
QY 544 CATGTAAACCAATCTGACAGATATACAGGAATCAGACCGACCAATTAAGAGCAAGAG 603
DB 541 CATATCGAATTTTACGCACTACACAGTTTCAAGCAACCAATTAAGCGCGCGGAGAG 600
QY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTAGAAGTGTGGTCCCGGG 663
DB 601 TTGGAGAGTATATGCTTAAACATTTTCGAAAGTACAGGAACAGCAATTAACAGGT 660
QY 664 GATTATACACCGCTTCCGGTGTTCAGAGCTGTATTTGAAAGACATCTAGACCG 723
DB 661 GGTATATCTCGCGCAGAACGTTTTGTCCGTCCGSCATCTTGAAAGAAATATTTAAAA 720
QY 724 GCGCGCATGAAACGAAAGGTATACAGCCGCTTTCAAAATTTGGCAAAATATAGCATA 783
DB 721 GCGAAAAACGAAAGAGCTATCAAAATGTGTATGTCTTGAACAGTGTCCGATT 780
QY 784 CCAAGGGCGCAGATGAAGAGAGAGAAATTCATTAACGATATCTTCCTGT 843
DB 781 CCGAATGAGCGGTAATTAAGAAAGTGTGACCTGATTTACACAAATATGTGGCATCT 840
QY 844 ATGTGCAACGAACTGGAATCTATTTCCACACTATGACAAATCGCAAAATCCAAAA 903
DB 841 ATGTGTTGCGAAGGCAAAAGCTACTTTTCACTCATACGAAACAAATCAATAGT 900
QY 904 GTAAATTTATTTCATGAAAGCTTGAAGCTTTGGA 938
DB 901 GTTACTTTGTCAAGAGGATTAAGAAATATGAA 935

RESULT 8
 ID ACA36885 standard; DNA; 990 BP.
 AC ACA36885;
 XX 19-JUN-2003 (first entry)
 DT
 XX Prokaryotic essential gene #18542.
 DE
 XX Antisense, ds. prokaryotic essential gene; cell proliferation;
 KM drug design; gene.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO200277183-A2.
 PD
 XX 03-OCT-2002.
 PF
 XX 21-MAR-2002; 2002WO-US009107.
 PR
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI: 2003-029926/02.
 DR P-PsDB: ABU33015.
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 24755; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway of
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the rest compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from Wipro at
 CC ftp.wipro.int/pub/published_pct_sequences
 XX

SO Sequence 990 BP; 347 A; 171 C; 215 G; 257 T; 0 U; 0 Other;
 Query Match 23.4%; Score 232.6; DB 8; Length 990;
 Best Local Similarity 53.0%; Pred. No. 4.7e-63;
 Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY	4	ATGTGACAGAGCTTTACATTGGAAGAACTGTCGACCGTTAAACATGTTATAGCAAGAACATG	63
DB	1	ATGTGACAGAGCTTTACATTGGAAGAACTGTCGACCGTTAAACATGTTATAGCAAGAACATG	60
QY	64	GATTTGATTTGAGCGGGGACAGAGGTATCTTATCCGCGCGTTACAGCTGGAAC	123
DB	61	GATTTGATTTATTTTGAAGCGAACCCCAACATTTAGCCCAAGAAATTTATGATGAGAA	120
QY	124	AGTGAAGCTGACGGAAGGGCCCATCAACACAGTACGCGTTATCGGTATGGGAGAA	183
DB	121	TCTTCTACAGACGATGCCAATATATTAATGATATGATGATTTGGAAGCGGAGAGAG	180
QY	184	CTTGAATATATATTTATTTGCGACGCGATTTATGAAGCGTTATCTTGTGCGCGCTT	243
DB	181	TTAGATTAATATCATTTTTCGACAGCGATTTGATGAAGAGATTAAGCTGTGCACTCTA	240
QY	244	TATTTTCCGGGCTATGCGAGATGAAGAAACGATTAAGGGAAGATACCGTTCACTGTC	303
DB	241	TATCTTCCAGAGAGAGCGTTATATGCGCACACACGAGGAGAGAAATCAATTTAGCT	300
QY	304	CCGATGAGTTTGTGACATGCGGTCTGTCAGTCTGTCAGTCTTTGGAAGAGCTAAAGAA	363
DB	301	CCAGAGAAATTTTGTCTTGTGCTGTATGGAACCTTGCCGACATTAAGATGTGAGACA	360
QY	364	AAGATTCGATCTTTACAGATTTGAGAGAAATTAATGATCTATTTGATACAGTTTACG	423
DB	361	AAGTATCGGTATTAATCACTTGATGATCAACAGTACCGTTACTGGAATCAACACCA	420
QY	424	CTTACCTGATATTTGTCAGCGGAGCGGCGGAAACCTGACATAGAACCAAGACAGAC	483
DB	421	TTACCTGATATTTTTCACAGACAGAGTGGGCTGTGTGATGATTTGAACCAAGAACCA	480
QY	484	GGCCTCAAGTCTATGATATCAACCTGTGTCTATGACGAAACAGCCCGACTTATATG	543
DB	481	TGCGTCTGATTAAGAAAGAAACCTGTGAGATTAAGCAATATGACGATCGAATG	540
QY	544	CATGTAACCAATTCGACCAATATACAGAAATCAAGCCGAACATTTAGAGCAAGAG	603
DB	541	CATATCGAAGATTTACGACATCACAGTTCATACAGCAACATTTAGCCGCGTGAAG	600
QY	604	ATGGCGGATTAAGCCCTTCTGCTTTGGCCAGGCTTAGAACTGTGTGCGCGGG	663
DB	601	TTGGAGGATATATGCTTAACCATTTTTCGAGGTACAGAAACAGCAATTTACAGGT	660
QY	664	GATTTATACACGCTTCCCGGTTGTGACAGCTGTTATTTGAAAGAACATTTAGACCG	723
DB	661	GATTTATCTCCGCCGCAAGAGTTTGTGCTGTGCGCATTTGAAAGAAATTTATMAA	720
QY	724	GCGCCGATGAAGCAAGAGGTATACACCGCTTTCAATTTTGGCAATTTGACGATA	783
DB	721	CGAAGAAACGAAAGAGAGCTATCACAATGTGTGTGTCTTAAACAGTGTCCGAT	780
QY	784	CCAAGGGCGGAGATTAACGGAAGAGACGAATTTCAATTAACCAATATATCTCCGT	843
DB	781	CGAATGAGCGGTATTTAAGAAAGTGTACCTGATTTCAACCAATATGTGGCAT	840
QY	844	ATGTGCAAGAAATCGAAACTACTATTTTCCACACTATGACATGCGCAATCCAAAA	903
DB	841	ATGTGTGGAAGAAAGCAAGCATATTTACCTCATGCAAAACCAACAAATCAATAGT	900
QY	904	GTAATTTATTTCAATGAGACCTTACGTTTGA	938
DB	901	GTTACTTTGTCAAGAAAGTTATGAATAATGAA	935

RESULT 9
 ADR89833

ID	ADNR89833standard; DNA; 1087 BP.
XX	
AC	ADNR89833;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Clostridium perfringens bile salt hydrolase gene.
XX	
KM	Bile salt hydrolase; enzyme; bile salt; cholesterol; encapsulation; gene;
XX	ds.
OS	Clostridium perfringens.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS 69..1058
FT	/*tag= a
FT	/product= "Bile salt hydrolase"
PN	WO2004076657-A2.
XX	
PD	10-SEP-2004.
XX	
PF	01-MAR-2004; 2004WO-CA000306.
XX	
PR	28-FEB-2003; 2003US-0450334P.
XX	
PA	(UTWC-) UNITV MCGILL.
XX	
PI	Prakash S, Jones ML;
XX	
DR	WPI: 2004-653417/63.
DR	P-PSDB; ADNR89834.
XX	
PT	Composition for decreasing target compound in gastrointestinal tract of
PT	animal, has biologically active agent that decreases target compound,
PT	reiner for retaining agent by contacting agent to limit movement of
PT	agent, and carrier.
XX	
PS	Claim 19; SEQ ID NO 7; 92pp; English.
XX	
CC	The present sequence is that of the gene encoding Clostridium perfringens
CC	bile salt hydrolase (BSH), an enzyme that catalyses the deconjugation of
CC	bile salts. The enzyme can be immobilised or encapsulated for use in a
CC	composition of the invention used to decrease the amount of bile acid in
CC	the gastrointestinal tract of an animal. A genetically engineered
CC	bacterium or cell expressing the BSH may also be used in the composition.
CC	The composition may also include a collector for collecting the by-
CC	product of bile acid deconjugation, deoxycholic acid. Deoxycholic acid
CC	may be captured e.g. by precipitation and collection in a capsule, where
CC	it is held until it is excreted. The compositions are useful for reducing
CC	bile and cholesterol levels in an animal to prevent or treat a disease or
CC	disorder characterised by increased bile or cholesterol levels, or a
CC	disease or disorder having increased bile or cholesterol as a risk
CC	factor, such as heart disease and cancer. The compositions are orally
CC	administered or implanted in the animal. The compositions are used in
CC	claimed methods of: lowering intraluminal bile acid of animals suffering
CC	from defective ileal transport of bile acids due to a congenital defect,
CC	resection of the ileum or a bowel disease or disorder; lowering serum
CC	cholesterol and/or total body cholesterol for the purpose of producing
CC	animal products of reduced cholesterol content; and to treat or prevent
CC	colon cancer. Immobilised or encapsulated BSH can also be used as an
CC	in vitro diagnostic tool for detecting liver or hepatobiliary disease in a
CC	patient by detecting and/or measuring bile acid degradation when
CC	contacted with a biological sample.
XX	
SO	Sequence 1087 BP; 427 A; 110 C; 187 G; 363 T; 0 U; 0 Other;
XX	
Query Match	19.7%; Score 196.4; DB 13; Length 1087;
Best Local Similarity	50.6%; Pred. No. 1.8e-51;
Matches 501: Conservative	0; Mismatches 486; Indels 3; Gaps 1

Db 68 ATGTGATGACAGGATTTAGCTTAGAAACAAAAGATGATTACATTTGTTGGAAACAAATAT 127

Qy 63 GGATTTTGCATTTTCAAGCTGGGGACAGAGGTGATTTCTCTATCCGGCCGTTACAGCTGGAA 122

Db 128 GGATTTTGAATTAATTCATTATTAATCAATCTATTATTAATTTATTTCTTAGGAATTTTAATGTG 187

Qy 123 CAGTGAAGCTACGGAAAGGGCCCATCAGACACAGTACGCGTTATCGGTATGGGAGAGAA 182

Db 188 AAACAAATCAACAAAAAAGAAATTTACACAAATATGCTGTTCTTGGAAATGGGAACATAT 247

Qy 183 ACTTGAATATATATTA---TTTGCCGACGGCATTTAATGAAGAAGCGTTATCTTGTCGGC 239

Db 248 TTTGATGATATATCTCACTTTGCAAGTGTATGAATGAAGAAGGATTTAGGGTGTGTCGG 307

Qy 240 GCTTATTTTCCGGGCTATGCGGAGTACGAAAAACGATACGGGAAGATACCGTTACAT 299

Db 308 CTTAATATTTCCCTGTTTATGTATGCTATTCCTAAAGAAAGATATGAAGGTAAACATAATAT 367

Qy 300 TGTCCCGCATGATTTGATGACATGGGGGCTGACAGTCTGCACTTTTGGAAAGCGTAA 359

Db 368 TCCAGTATATATTTCTTATTTATGGGTTTAACTAATTTAGCTCAGTAGAAGGGTAA 427

Qy 360 AGAAAGATTCGATCTTTAAGCATTTGAGAGAAAAATTAATGATCTAATTTGATACAGTTT 419

Db 428 GGAAGCAATTAATAAATGCTAATATATAGTGAATATACCATTTAGGAAAAATATCTCTAATAC 487

Qy 420 ACCGCTTCACTGATTTGTCAGACCGGACGGCCCGAAACCTGACGATAGAACCAAGAC 479

Db 488 AACTCTTCATTTGATGATTAAGCGATTAACAGAAAGTCTAATTTGTGGTTGAACAAACAA 547

Qy 480 AGAGGGCTCAAGTCTATGATATATCAACTGGTGTCTATGACGACAGCCCGACCTTAT 539

Db 548 GGAATAATTAATGATATTTATATATATATATGAGATTAATCAATTAATTCACCTTATTTGA 607

Qy 540 ATGCACTGATACCAATCTGACAGCAATTAACAGAAATCAACCGAAGCAATTAGAGACAA 599

Db 608 TTGGCAGTGAACAAATTTAATCAATATGATGATGATGATATATATCAATGATTCAGAAAT 667

Qy 600 AGAGATGGCGGATTTAGCCCTTTCTGCTTTTGGCCAAAGCTTAGAACTGTGTGCTGCC 659

Db 668 TAAGTTAGAGATCAATCTTTAATCTGCTTAGGTCAGAGAACTGTATTAGGATTAAC 727

Qy 660 GGGGATTTATACACCGCTTCCCGGTTTGCACAGCTGTTATTTGAAAGAACATCTAGA 719

Db 728 AGGGAGCTTTACCTGTCATCTAGATTTATMAAGTAGACATTTTAAAGATGCAATGAT 787

Qy 720 GCCGGCGCGATGAAACGAAAGGTGTAACGCGCTTTCAATTTTGGCAATATGAC 779

Db 788 AAAAAATGATTAAGATTCATTAAGATCTTAATTTTTCATATATTAATATATATATGTTGC 847

Qy 780 GATACCAAGGGCGCATGATTAACGAGAGAGACGAATTCATTAATACGCAATATATCTTC 839

Db 848 TATGTTAAGAGATCACTAGAACTGTAAGAGAAAAAGATGATCTTACTCAATATATCAAG 907

Qy 840 CGTATGTGCAAGAACTGGAACTATCTATTTCCACCACTATGACAAATCGGCAATCCA 899

Db 908 TTGATCTGTGTTGAAAGAAAGAAATTTATTTATTTAATACCTAAGAAATATCAAAATTA 967

Qy 900 AAAAGTAAATTTATTCATGAAGAACCTTGACTGTGTTGAGCCCTAAGTGTGTTCCGCTAA 959

Db 968 TGCATATGACATATTAAGAAAACTTAGATGGAATTAAGAAATTAACATATTAATTAACA 1027

Qy 960 AGCAGAGAGATGATTCATGAGCTTAATTA 989

Db 1028 CAAAATTTTAAGTATTAATCAATGTAATTA 1057

RESULT 10
ABA90521.18/c
Continuation (19 of 24) of ABA90521 from base 180001 (Genomic sequence of Lactococcus
MP Sequence split into 24 fragments LOCUS ABA90521 Accesion ABA90521
Fragment Name Begin End
MP ABA90521.00 1 110000

Query Match 17.8% Score 177; DB 6; Length 110000;
 Best Local Similarity 50.8%; Pred. No. 3.2e-44;
 Matches 504; Conservative 0; Mismatches 480; Indels 9; Gaps 3;

WP	ABA90521_01	100001	210000
WP	ABA90521_02	200001	310000
WP	ABA90521_03	300001	410000
WP	ABA90521_04	400001	510000
WP	ABA90521_05	500001	610000
WP	ABA90521_06	600001	710000
WP	ABA90521_07	700001	810000
WP	ABA90521_08	800001	910000
WP	ABA90521_09	900001	1010000
WP	ABA90521_10	1000001	1110000
WP	ABA90521_11	1100001	1210000
WP	ABA90521_12	1200001	1310000
WP	ABA90521_13	1300001	1410000
WP	ABA90521_14	1400001	1510000
WP	ABA90521_15	1500001	1610000
WP	ABA90521_16	1600001	1710000
WP	ABA90521_17	1700001	1810000
WP	ABA90521_18	1800001	1910000
WP	ABA90521_19	1900001	2010000
WP	ABA90521_20	2000001	2110000
WP	ABA90521_21	2100001	2210000
WP	ABA90521_22	2200001	2310000
WP	ABA90521_23	2300001	2365589

Query Match 17.8% Score 177; DB 6; Length 110000;
 Best Local Similarity 50.8%; Pred. No. 3.2e-44;
 Matches 504; Conservative 0; Mismatches 480; Indels 9; Gaps 3;

QY	7	TTGCACAGCTTACATTGGAACCTGCTGACCGTAAACATGATTTAGCAAGAACATGAT	66
DB	104062	TGTACTAGTTTACACTAGAGATCAAGATTAATTAATTTCTTCTGTCATTAATGAT	104003
QY	67	TTTGATTTACGCTGGGACAGAGGTGATCTCTATCCGCG---CCGTTACGCTGAAC	123
DB	104002	TTTCAATAAGAAATGCGGAAACAAATCTTTTATTCAGAAACAGAGATAGGATTT	103943
QY	124	AGTGAAGCTGACGGAAGGCGCCATCAGACAGTACGCGTTATCGTATGCG---GAGA	180
DB	103942	GCCCACTTAAGAAAGACATTTGAAACATCTTAATGCTTTGTTGGATGGGTGCGATG	103883
QY	181	AACTTGAATATATTTATTTGCCAGCGCATTAATGAAGCGGTTATCTTGCGGCG	240
DB	103882	GAAAGGGGCGATCCAGTACTCTTGTATGATCAACGAAAGGTTAATGGGTGCGACT	103823
QY	241	CTTATTTTCCGGGCTATGCGAGTACGAAAGATACCGGATACCGTTCACTT	300
DB	103822	TGTATTTCCAGGCTATGCTGATGATGATATCAAAAATCAAAAGGAAAT	103763
QY	301	GTCGCGCATGATTTGTGACATGGGTGCTGCTGATCTGTCAGTCTTGGAGACGTAAA	360
DB	103762	TCACTGATATGTTTATTCACAGGTCTCTCACTCAAGCGAGTATTTAGAAAGAAATCTT	103703
QY	361	GAAAGATTCGATCTTTAAGATTTGAGAAAAAATGATCTA---TTGATACAGTT	417
DB	103702	GATTTATTTGATPAAAAATTTGTTATTAATTAATGATACATCAACCTTAGGTCCTACG	103643
QY	418	TTACCGCTTCACTGATTTGTCAGACCGGACGGCGGAAACCTGACGATGAGAACCAAGA	477
DB	103642	CCTCTTTTCAATTTATTTTCTGATTTCTAGTGGTCAAGTTGATTTATGACCAAGG	103583
QY	478	GCAGACGGCTCAAACTATGATTAATCAACTGTGTCTATGACGAAACGCGGACCTTT	537
DB	103582	CAAGTGACCTTTCAATTAATAAAGATTCATTTGATGATGACAAATGTCAGATAC	103523
QY	538	ATATGGCATGTAAACCAATCTGACCAATATACAGAAATCAAGCCGAGCAATTAAGAGC	597
DB	103522	CAATGCGACGAAACTATTAATTAAGAAATTAATCTTTTCACTTAATCAAAAGAAAGT	103463
QY	598	AAAGATGGGCGGATTAAGCCCTTTCTGCTTTTGGCCAGGCTTAGAAACTGTGTCTG	657
DB	103462	ATCGAACTTTAGAAAGACATTAACATTTATGTCAGGTTCAAGTACTTTTGGATTT	103403
QY	658	CCGGGGATTAATACACCGCCTTCCGGTTTGTACAGAGCTGTTATTTGAAAGAACATCTA	717

Query Match 17.8% Score 177; DB 6; Length 110000;
 Best Local Similarity 50.8%; Pred. No. 3.2e-44;
 Matches 504; Conservative 0; Mismatches 480; Indels 9; Gaps 3;

DB	103402	CCAGAGATTTTACACCTCTTCAAGATTTGTTGAACGCTTATTTAAAAAATACGCT	103343
QY	718	GAGCGGCGGCGCGATGAAACGAAAGGTGTACACGCGCTTTTCAATTTTGGCAAAATAG	777
DB	103342	GAGAAACCAAGTATTAATTAATTAAGCGGCTATTAAGCTTTGATCATATTAATGAAATCTGTA	103283
QY	778	ACGATACCAAGGCGCGATGATTAAGGAAAGAGCAAAATTCATTAATGCAATATACCT	837
DB	103282	ATTAATTCAAAAGAAATGTTATTAATGAGCATGAGACGAAAGTATTCATCTGTTATTCG	103223
QY	838	TCCGATGTCGACGAAACCTGGAATCTATTTCCACCACTATGACCAATCGGAAATC	897
DB	103222	GCAATATATGCTCTCAAGAACTTAATTAATTTTCACTTAATGATTAACAAAGAAATC	103163
QY	898	CAAAAGTAATTAATTAATTAATTAAGACCTTGAACCTTGAACCTTGAACCTTGAACCTT	957
DB	103162	AGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	103103
QY	958	AAAGCAGAAAGAGTATTCATGAGCTTAATTA 990	
DB	103102	GTCATGAGAAAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	103070

Query Match 17.8% Score 177; DB 6; Length 110000;
 Best Local Similarity 50.8%; Pred. No. 3.2e-44;
 Matches 504; Conservative 0; Mismatches 480; Indels 9; Gaps 3;

QY	7	TTGCACAGCTTACATTGGAACCTGCTGACCGTAAACATGATTTAGCAAGAACATGAT	66
DB	104062	TGTACTAGTTTACACTAGAGATCAAGATTAATTAATTTCTTCTGTCATTAATGAT	104003
QY	67	TTTGATTTACGCTGGGACAGAGGTGATCTCTATCCGCG---CCGTTACGCTGAAC	123
DB	104002	TTTCAATAAGAAATGCGGAAACAAATCTTTTATTCAGAAACAGAGATAGGATTT	103943
QY	124	AGTGAAGCTGACGGAAGGCGCCATCAGACAGTACGCGTTATCGTATGCG---GAGA	180
DB	103942	GCCCACTTAAGAAAGACATTTGAAACATCTTAATGCTTTTGGATGGGTGCGATG	103883
QY	181	AACTTGAATATATTTATTTGCCAGCGCATTAATGAAGCGGTTATCTTGCGGCG	240
DB	103882	GAAAGGGGCGATCCAGTACTCTTGTATGATCAACGAAAGGTTAATGGGTGCGACT	103823

QY 481 GAGGCGCTCAAGTCTATGATATCAACCTGTGTGATGAGACAGCCGCACTTATA 540
 DB 815 ACAGGCACTTACATTCATCGAAAACGATTGGCTCTATGAGAAATGCCCTGTATGAA 874
 QY 541 TGGCATGTAACCAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAGAGACAAA 600
 DB 875 TGGCATGTAACCAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAGAGACAAA 934
 QY 601 GAGATGGCGGATGAGCCCTTCTGCTTTGGGCAAGGCTTAGAACCTGTGGCTGCG 660
 DB 935 ATGATGGAGACTTGTGATTTGACACCGTTGGGCAAGGCGGCTTAGAGATTACCA 994
 QY 661 GGGGATATACACCGCTTCCCGTTGTCTGACAGCTGTTATTTGAAAACATCTAGAG 720
 DB 995 GGTGATTTTACGCGCTGACGACGTTTCTTGGGTAGACATCTGAAAAAATATACGAA 1054
 QY 721 CCGGCGGCGGATGAAACGAAAGGTGTAAACAGCCGCTTTCAAAATTTGGCAATATGACG 780
 DB 1055 AAAGCCAAATGAAACGAAAGGCGTAAACAACTGTTCATATCTTCTGTAAAT 1114
 QY 781 ATACCAAAAGGCGGATGATACGGAAGAAACGAAATTCATTTACGCAATATCTTCC 840
 DB 1115 ATCCCAAAAGGTGTGTTTGAACAAATGAGGGAACGAAATTAACCTATATCTCA 1174
 QY 841 GTGATGTGCAACGAACTGAAACTACTATTTCCACCACTATGACAAATCGGCAATCCAA 900
 DB 1175 GCTATGTGTGCAACAAAGTAAACTATTTAACTGTATGACAAATGTCGAATTTCA 1234
 QY 901 AAAGTAAATTTATTTATGATGAAAGCTGTGCTGTGGAGCTTAAAGTGTTCGCTTAA 960
 DB 1235 GCCGTTTCCTTAATGCTGAAATTTAAATGTCAGATTTAATTAATCAATTGAGTGGAT 1294
 QY 961 GCAGAAAGACTATTCATGACTTAATTAAGA 993
 DB 1295 GCTAAACAAATTAATTAAGCAATTAATCAAGTA 1327

RESULT 13
 ID ADJ62865 standard; DNA; 1616 BP.

AC ADJ62865;
 DT 06-MAY-2004 (first entry)
 XX B sphaericus penicillin-V-amidase gene related to cancer treatment.
 XX beta-catenin; bipartite T-cell factor; Tcf; promoter construct; Lef-1;
 KM cytoskeletal; beta-catenin activity inhibitor; gene therapy; colon cancer;
 KM metastasis; liver; thymidine kinase; prodrug; chemotherapy;
 KM radiation therapy; surgery; penicillin-V-amidase; gene; ds.
 XX Bacillus sphaericus.
 OS US200328285-A1.
 PN 11-DEC-2003.
 PD 05-MAY-2003; 2003US-00429802.
 PF 03-MAY-2002; 2002US-0377672P.
 PR (HUNG/) HUNG M.
 PA (KMON/) KMONG K Y.
 PA (ZOU/) ZOU Y.
 XX Hung M, Kwong KY, Zou Y;
 PI WPI, 2004-042209/04.
 DR Novel viral vector comprising beta-catenin/bipartite T-cell factor-
 PT responsive promoter having first and second promoter region linked to

PT target nucleic acid sequence, useful for treating cancer.
 XX disclosure; SEQ ID NO 17; 114pp; English.

CC This invention relates to a novel viral vector comprising a beta-
 CC catenin/bipartite T-cell factor (Tcf)-responsive promoter construct which
 CC contains a first promoter region having a copy of Tcf/LEF-1 binding site
 CC operatively linked to a second promoter region, and a nucleic acid
 CC sequence, where the first and second promoter regions are operatively
 CC linked to target nucleic acid sequence. The invention may be useful for
 CC the development of compounds with a cytostatic activity, through action
 CC as beta-catenin activity inhibitors, or for gene therapy. The invention
 CC may be useful for treating an individual with colon cancer which is
 CC metastasized to the liver. The treatment involves administering the
 CC vector of the invention where the nucleic acid sequence encodes a
 CC therapeutic polypeptide or thymidine kinase, a prodrug and chemotherapy,
 CC radiation, surgery or gene therapy to the individual. The present
 CC sequence is that of a therapeutic gene which may be used in the vector of
 CC the invention for the treatment of an individual with cancer.

XX Sequence 1616 BP; 549 A; 244 C; 319 G; 504 T; 0 U; 0 Other;

Query Match 17.4%; Score 173.8; DB 12; Length 1616;
 Best Local Similarity 49.8%; Pred. No. 3.6e-44;
 Matches 495; Conservative 0; Mismatches 492; Indels 6; Gaps 2;

QY 7 TGCACAGCTCTTACATTTGAAAGCTGTGACCGTAAACATGATATAGCAAGAAACATGAT 66
 DB 335 TGCAGTATGCTTATCAATTCGTACACAGATGATAAAGTTATTCGCTCGCAATGAT 394
 QY 67 TTTCATTTTCACTGGGGAACAGAGTATCTCTATCCGGCGCTTACAGTGAACAGT 126
 DB 395 TTTCATTTTCACTGGGGAACAGAGTATCTCTATCCGGCGCTTACAGTGAACAGT 454
 QY 127 GAGGTGACGGA---GGGCCATCAGACAGTACGCGTTATCGGTATGGGAGAA-- 181
 DB 455 TTGAAAAAGAAATGATGATTTACATTTACATTTACATTTGTTGGAATGGAAAGCACT 514
 QY 182 -AAGCTGAAATATATTTATTTGCGAGCGCATTAATGAAAGCGTTATCTTGTGGCGG 240
 DB 515 GACATTTACATCAGACGTTCTCTATGATGGGTAAACGAAAGGATTAATGGGCGCATG 574
 QY 241 CTTTATTTTCCGGCTATGCGGATACGAAAAACATACGGAAGATCCGTTCACTT 300
 DB 575 CTTTATTTTCCGGCTATGCGGATACGAAAAACATACGGAAGATCCGTTCACTT 634
 QY 301 GTCCGATGAGTTTGTGACATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 635 AATCCGCTGATGATTTCTCAAGTTTGAAGAAATTTGTAATTTGTAATTTGTAATTT 694
 QY 361 GAAAGATTCGATCTTTAGCATTTGAGAAAAAATTAATTAATTTGTAATTTGTAATTT 420
 DB 695 GAAAGATTCGATCTTTAGCATTTGAGAAAAAATTAATTAATTTGTAATTTGTAATTT 754
 QY 421 CCGCTTCACTGATATTTGACACCGGACCGGCGGAAACCTGAGATGAAACCAAGACA 480
 DB 755 CCACCTTCACTGATATTTGACATGCTTGTGTAATTCGATTTGTAATTTGTAATTT 814
 QY 481 GAGGCGCTCAAGCTTATGATATCAACCTGTGTGATGAGCAAGCCGCACTTTTATA 540
 DB 815 ACAGGCACTTACATTCATCGAAAACGATTGGCTCTATGAGAAATGCCCTGTATGAA 874
 QY 541 TGGCATGTAACCAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAGAGACAAA 600
 DB 875 TGGCATGTAACCAATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAGAGACAAA 934
 QY 601 GAGATGGCGGATGAGCCCTTCTGCTTTGGGCAAGGCTTAGAACCTGTGGCTGCG 660
 DB 935 ATGATGGAGACTTGTGATTTGACACCGTTGGGCAAGGCGGCTTAGAGATTACCA 994
 QY 661 GGGGATATACACCGCTTCCCGTTGTCTGACAGCTGTTATTTGAAAACATCTAGAG 720
 DB 995 GGTGATTTTACGCGCTGACGACGTTTCTTGGGTAGACATCTGAAAAAATATACGAA 1054

QY	721	CCGGGGGCGS	ATGAACGAAAGAGTGTAA	CAGCGCTTTT	CAAAATTGGCAAATATGAC	780
Db	1055	AAAGC	AAAAAATGAAACAGAAAGCGTAA	CAAACTGTTC	CAATCTCTCTTAAT	1114
QY	781	ATACCA	AAAGGCGCAGTGTAA	CGAAGAAAGCAATTCATTA	TATACCAATATCTCC	840
Db	1115	ATCCCA	AAAGGTGTGTTTTG	CAATGAGGGGAAACGSA	TTATACCATCTATCTCA	1174
QY	841	GTGATGTG	CAACGAAACTGAAACTACTATTTCC	ACACTATGACAAATCGGAAATCC	CA	900
Db	1175	GCTATGTG	CACAAAGTAAACCTATTA	CTTTAACTGTATGACAAATGTCGAATTTCA		1234
QY	901	AAAGTAA	ATTATTTTCATGAAGACCTTGA	CTGTTTGAGCC	TAAAGTGTTTTCCGCTAA	960
Db	1235	GCCGTTT	CCTTAATGCTGAAATTTA	TATATAGTCAAGATTTA	TATACATTTGAGTGGAT	1294
QY	961	GCAGAG	AGAGATTCATGAGCTTA	TTAAAGA		993
Db	1295	CGTAA	CACAGATATTAGCAATTA	ATAACAGTA		1327

	RESULT 14
XX	ACAA6430
XX	ID ACAA6430 standard; DNA; 978 BP.
XX	ACAA6430;
XX	19-JUN-2003 (first entry)
XX	Prokaryotic essential gene #28087.
XX	DE Prokaryotic essential gene #28087.
XX	KM Antisense; ds; prokaryotic essential gene; cell proliferation;
XX	KM drug design; gene.
OS	Staphylococcus epidermidis.
XX	WO200277183-A2.
PN	03-OCT-2002.
XX	PD
XX	PF 21-MAR-2002; 2002WO-US009107.
XX	PR 21-MAR-2001; 2001US-00815242.
XX	PR 06-SEP-2001; 2001US-00948993.
XX	PR 25-OCT-2001; 2001US-0342923P.
XX	PR 08-FEB-2002; 2002US-00072851.
XX	PR 06-MAR-2002; 2002US-0362599P.
PA	(ELIT-) ELITRA PHARM INC.
XX	Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW;
PI	Mall D, Tramwack JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI	WPI; 2003-029926/02.
DR	P-PDB; AB042560.
XX	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
PS	Claim 14; SEQ ID NO 34300; 1766pp; English.
XX	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	to the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) required for proliferation, or that inhibits cellular proliferation; (9) identifying a gene required for cellular proliferation; (10) a biological pathway in which a proliferation-regulated gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences

Query Match	16.1%;	Score 160.2;	DB 8;	Length 978;
Best Local Similarity	49.9%;	Pred. No. 6.1e-40;		
Matches 458;	Conservative 0;	Mismatch 453;	Indels 6;	Gaps 2;
QY 4	ATGTCGCAAGTCTTACATTGSAACACGCTGACCGGTAAACATGATTAGCAAGACATG	63		
Db 1	ATGTCGCAAGTCTTACATTGSAACACGCTGACCGGTAAACATGATTAGCTGACGATG	60		
QY 64	GATTTCGATTTCAGCTGGGGAACAGAGTGATTCCTATCCGCGCGTTACAGCTGGAAC	123		
Db 61	GACTTCGATTTCGATTTCAGCTGGGGAACAGAGTGATTCCTATCCGCGCGTTACAGCTGGAAC	120		
QY 124	AGTGAAGCTACCGAAGGCGCCATCAGACACAGTACCGCTTATCGGTATGGGAGAAAA	183		
Db 121	TTTGATCTCAATTC--GACATGCGCTTGAATATGTTGTTGGACAAATTTTAAAA	177		
QY 184	CTTGGAAATATATATATTTGCGCAACGACATTAAGAAACGGTTATCTGTGCGCGCTT	243		
Db 178	GTAGACGTTATAGATTGGTGTATGATTAAGAAAGTTTACGCTATTTCCAAACAT	237		
QY 244	TATTTCCGGGCTATGCGAGTACGAAAAACGATACGGGAAGTACCGTTCATTTGTC	303		
Db 238	TACTTCACGTGAGCGCTCATACAGTACCATTAACGTTATGGTATTTTAACTTAGCA	297		
QY 304	CCGCAATGATTTGTGACATGGGTCTCATGCTGTCACTTTTGGAAACGTAAAAAA	363		
Db 298	CCGAGAGATTTATGTTGGGTTTATGTTTAAATTAAGTATTAAGCAATTTAAAAAA	357		
QY 364	AAGATTGCATCTTAAACGATTGTAGAGAAAAAATTAAGTCTATTTGATACAGTTTACG	423		
Db 358	AAGGTTAAGAGATCAATATTATGAATGAAAAAATTAACAATTGAATATCGTCTCT	417		
QY 424	CTTCACTGATATTTGTACAGCCGACGGCGCGAACTGACGATAGAACCAAGACAGAC	483		
Db 418	TTTCAATTTATGCTCATGATGAAGACGACATACGTAACCTTAGAACCTCAAAATGGC	477		
QY 484	GGCCTCAAGTCTATGATTAATCACTCGTGTGATGACGACAGACCCCGACTTTATATGG	543		
Db 478	TTATTAATAGTTAAAGATATATTTGTTCACTTAAACAATCGCCTTAATTAATGATTTGG	537		
QY 544	CATGTACCAATGTGACAGATTTACAGAAATACAGCCAGAGAAATTAGAGCAAGAGAG	603		
Db 538	CATCTATCTAATTAAGAAATATGCTTATTTTAAACCAACAGAAATCAACCAATCAATTA	597		
QY 604	ATGGGCGGATTAAGCCCTTTCTGCTTTGGCCAAAGGCTTATGGAATCTGTGCGCGGG	663		
Db 598	ATAGTGAAGTGTATGAATGAATCAATGGGTGTGAAGCAGAAACAAATGGCTTAACGGGT	657		
QY 664	GATTATACACCGCTTCCGGTTTGTCAAGCTGTTTATTTGAAGAACATCTAAGCCG	723		

Db 658 GGTATATCTTCAACAGACGTTTATACGGGCTACATTTTAAAGCACCACTACGCTGT 717
Qy 724 GCGGCCCATGAAAGAAAGGTGTAAACAGCCCTTTCAAAATTTGGCAAAATATACATA 783
Db 718 TCCCATATGAAAGTAAATTTATGAAATTTTAAAGTTCTAGATCAGTACATC 777
Qy 784 CCAAGGGCCGATGATTAACGAAAGACGAAATTCATTAAGCAATATACCTTCCGTG 843
Db 778 CTTCAAGGTGAGATTAT---CGATGCCAATTAATACCTTACACACATATCATTTAGTG 834
Qy 844 ATGTGCAACGAAGTGAAGTACTATTTCACCACTATGACAAATCGGCAATCCAAA 903
Db 835 ATGAAAGTAAAGAAAGACCTATTATTAAGCAGATCTTAGTAATCAATTTTCAA 894
Qy 904 GTAAATTTATTTTCATGA 920
Db 895 ATAAATTTACTGAGA 911

RESULT 15

AAH52510 standard; DNA; 990 BP.

AAH52510;

03-SEP-2001 (first entry)

S. epidermidis open reading frame nucleotide sequence SEQ ID NO:413.

Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis; de.

Staphylococcus epidermidis.

MO200134809-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US030782.

09-NOV-1999; 99US-0164258P.

(GLAXO) GLAXO GROUP LTD.

Kimmerly WJ;

WPI; 2001-316495/33.

P-PSDB; AAG81660.

Nucleic acid encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

Claim 8; Page 151-152; 2188pp; English.

AAH52304 to AAH5970 represent nucleic acid (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acid (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given

CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464

SO Sequence 990 BP; 361 A; 158 C; 158 G; 313 T; 0 U; 0 Other;

Query Match 16.0%; Score 159; DB 4; Length 990;

Best Local Similarity 49.8%; Pred. No. 1.5e-39;

Matches 459; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Qy 2 ATATGCGCAAGATCTTACATGGAAGACGCTGACGCTTAACATGATTAAGCAAGACAA 61
Db 8 ATATGCTACTGCAATTTCTTTATATCAAAACAGCTTACATATTTAGTGAACAA 67
Qy 62 TGAATTTGCAATTTACGCTGGGACAGAGGTGATTCATATCCGCGCTTACAGCTGA 121
Db 68 TGGACCTTGCAATTTGATTTAATGATATCCCAACATGTTTCCACGCGCATATACATACC 127
Qy 122 ACAATGAGCTGACGGAAGGCGCCATACACAGATGCGCTTATGCGTAATGGGAGAA 181
Db 128 AATTTGATCTAGATTCAGACATGCGTCTT---GAATATGATTTGTTGAAACAATTTAA 184
Qy 182 AACTGGAATATATATTTATTTGCGAGCGCATTAATGAAAGCGTTTATCTTGCGCGC 241
Db 185 AAGTAGACGTTATAGATTTGATGATGTTAAACAAAAGTTTACGTTATTCGAAC 244
Qy 242 TTTATTTCCGCGCTATGCGAGTACGAAAAAAGATACGGAAGATACCGTTACATTTG 301
Db 245 ATTAATTTCACTGATGGAAGCTCATACAGTACCATTAACGTTATGTTATTTAACTTAG 304
Qy 302 TCCGCAATGATTTGACATGCGTGTGCTGATCTGATCTGCTTTGAAAGACGTAAAG 361
Db 305 CACCTGAGAGTTTATGTTTGGTTTATGTTTAAATTAAGATTAAGCAATTAAC 364
Qy 362 AAAAGATGATCTTTAAGATTTGAGAAAAAATAGATCTATGATACAGTTTAC 421
Db 365 AAAAGTTAAGAAATATATATTAATGATTAATGAAAAAATAGACCTTTGAATTCCTC 424
Qy 422 CGCTTCACTGATATTTGTCAGACGCGCGCGAAACCTGACATTAAGAACAGACAG 481
Db 425 CTTTACATTTCAATGATGATGAAACAGACATACCGATGAAAGCTCACATG 484
Qy 482 ACGGCTCAAAAGTCTATGATTAATCAACCTGTGTCATGAGAACAGCCGACCTTATAT 541
Db 485 GCTTATTAATGATTAAGATTAATTAATGATTAATTAATTAATTAATTAATTAATTA 544
Qy 542 GGCATGTAACCAATCTGACAGCAATATACAGAAATCAGACGGAATTAAGAGCAAG 601
Db 545 GGCATCTATCTTAATTAAGAAATTAACCTTTTAAAGCCACAGAAATCAACCAATCAT 604
Qy 602 AGATGCGCGATTAAGCCCTTTCTGCTTTTGGCCAAAGCTTAAGAACTGTGTGCGCG 661
Db 605 TAATAGTAAAGTCTGTAAGATTAATGATGCGCTGTGAAGCAAGAACTGTTACCGG 664
Qy 662 GGCATTAACACGCGCTTCCCGGTTGTCAAGCTGTTATTTGAAAGAACATTTAGAGC 721
Db 665 GTGCTTATAGCTCAACAGATGTTTATTAACGCGCTATATTTAAGACACCAACTAGCGT 724
Qy 722 CCGGCGCGCAATGAAGAAAGGTGTAACAGCGCTTTCAATTTGGCAAAATTAAGACA 781
Db 725 GTTCCATTAAGAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 784
Qy 782 TACCAAGGCGCGATTAAGCAAGAAAGCAATTCATTAATGCAATTAATTCGCG 841
Db 785 TCCCTCAAGGTGAGATTAT---CGATGCCAATTAATTAATTAATTAATTAATTAATTA 841
Qy 842 TGAATGCAAGAACTGGAATCTATTTTCCACGCTATGACAAATCGGAATTCCAA 901
Db 842 TGAATGCAAGAAAGTAAAGAAAGTATTAATTAATTAAGCTTATTAAGCAATCAAAATTTCA 901
Qy 902 AAGTAATTTATTTTCATGA 920
Db 902 AATTAATTTACTGAGA 920

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Page 15

Search completed: March 18, 2006, 12:55:34
Job time : 654 secs

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2006, 11:46:51 ; Search time 4766 Seconds

(without alignments)
9777.577 Million cell updates/sec

Title: US-10-812-387-1

Sequence: 1 catatgtgcacaagctctac.....atgagcttaataagaatcc 996

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	85.8	8.6	595	9 BH861030	BH861030 297 Lste
C 2	45.2	4.5	853	10 CZ540175	CZ540175 SRA-aad3
C 3	44.6	4.5	175	8 CV973894	CV973894 DPF370 Bt
C 4	44.6	4.5	881	9 AZ533653	AZ533653 ENTCS21R
C 5	44.6	4.5	910	9 AZ538681	AZ538681 ENTFO61R
C 6	44.6	4.5	923	9 BH155642	BH155642 ENTSS56TR
C 7	41.4	4.2	842	9 AZ688508	AZ688508 ENT1247TR
C 8	41.4	4.2	871	9 AZ683787	AZ683787 ENTUK64TR
C 9	39.6	4.0	773	10 CZ859348	CZ859348 OC_Ba025
C 10	39.4	4.0	1055	9 CC254220	CC254220 CH261-4N2
C 11	38.6	3.9	512	9 BH059630	BH059630 RPCI-24-3
C 12	38.2	3.8	1101	10 CR008507	CR008507 Drosophila
C 13	38.2	3.8	575	11 CR008507	CR008507 Drosophila
C 14	38.2	3.8	593	3 BQ266623	BQ266623 NISC FF14
C 15	38.2	3.8	853	9 AZ669903	AZ669903 ENTHT10TR
C 16	38.2	3.8	859	9 AZ691994	AZ691994 ENTUN63TR
C 17	38.2	3.8	881	9 AZ546452	AZ546452 ENTTP78TR
C 18	38.2	3.8	918	9 AZ686647	AZ686647 ENTIO56TR
C 19	38.2	3.8	929	9 BH149784	BH149784 ENTQD08TR
C 20	38	3.8	286	2 BH123826	BH123826 I029P41P
C 21	38	3.8	534	9 BH745272	BH745272 gU78C09.B
C 22	38	3.8	632	2 BB661316	BB661316 BB661316

23	38	3.8	678	4 AK085491	AK085491 Mus muscu
C 24	38	3.8	809	9 BH576107	BH576107 BOHNN15TR
C 25	38	3.8	997	5 BX838785	BX838785 BX838785
C 26	37.8	3.8	700	9 BH969780	BH969780 odc08606
C 27	37.6	3.8	625	9 BZ348527	BZ348527 hps8e09.g
C 28	37.6	3.8	670	9 CE125413	CE125413 C1gr-g8e
C 29	37.4	3.8	674	9 CC535077	CC535077 C1gr-g8e
C 30	37.2	3.7	953	10 CL089852	CL089852 ISB1-14B1
C 31	37	3.7	439	7 CV163210	CV163210 rsmmx1.00
C 32	37	3.7	403	1 AA190615	AA190615 zq44d03.r
C 33	37	3.7	606	10 CL326680	CL326680 RPCI44.24
C 34	37	3.7	713	9 BH97867	BH97867 oe87d0I.
C 35	37	3.7	853	10 AG419422	AG419422 Mus muscu
C 36	36.8	3.7	197	11 CR829657	CR829657 GR0AA61C
C 37	36.8	3.7	427	1 AM829989	AM829989 ra48f01.y
C 38	36.8	3.7	435	1 AM829982	AM829982 ra48f03.y
C 39	36.8	3.7	482	1 AM735552	AM735552 ra21g07.y
C 40	36.8	3.7	505	1 AM783263	AM783263 ra26f02.y
C 41	36.8	3.7	505	1 AM783425	AM783425 ra28f01.y
C 42	36.8	3.7	505	1 AM828979	AM828979 ra70d09.y
C 43	36.8	3.7	505	1 AM828980	AM828980 ra70d10.y
C 44	36.8	3.7	505	1 AM828992	AM828992 ra70e11.y
C 45	36.8	3.7	505	1 AM829000	AM829000 ra70f07.y

ALIGNMENTS

RESULT 1
BH861030/c
LOCUS
DEFINITION
297 Listeria monocytogenes PUC18 library Listeria monocytogenes genomic clone 10-94 similar to Penicillin acylase/contagated bile hydrolyase and glutamate decarboxylase (adjacent Listeria monocytogenes ORF6), genomic survey sequence.

ACCESSION
BH861030
VERSION
BH861030.1 GI:28317960
KEYWORDS
GSS.
SOURCE
Listeria monocytogenes
ORGANISM
Listeria monocytogenes
REFERENCE
1 (bases 1 to 595)
Call,D.R., Borucki,M.K. and Besser,T.E.
Mixed-genome microarrays reveal multiple serotype and lineage-specific differences among strains of Listeria monocytogenes
JOURNAL
J. Clin. Microbiol. 41 (2), 632-639 (2003)
PUBMED
12574259
COMMENT
Contact: Monica Borucki
Animal Disease Research Unit
USDA-ARS
3003 ADRF, WSU, Pullman, WA 99164, USA
Tel: 509 335 7407
Fax: 509 335 8328
Email: mborucki@vetmed.wsu.edu
PCR Primers
FORWARD: M13F
BACKWARD: M13R
Insert Length: 595 Std Error: 0.00
Seq primer: M13F, M13R
Classes: plasmid ends.

FEATURES

source
1..595
/organism="Listeria monocytogenes"
/mol_type="genomic DNA"
/strain="multiple"
/db_xref="taxon:1639"
/clone="10-94"
/clone_lib="Listeria monocytogenes PUC18 library"
/note="Vector: pUC18; Shotgun library prepared by Amplicon Express (Pullman, WA)"
ORIGIN

Query Match 8.6%; Score 85.8; DB 9; Length 595;
 Best Local Similarity 54.6%; Pred. No. 6,6e-14;
 Matches 171; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 626 CTTTGGCCAGGCTTGAAGACCTGTTGCTGCGGCGGATTAATACACCGCTCCCGGT 685
 |||||
 DB 590 CATTTTCGACAGGATACAGAAACAAATTAACAGGATGTTATATCCGCGCAACGTT 531
 |||||
 QY 686 TTGTCAGAGCTGTTATTTGAAACATCTAGACCGCGCGCGATGAAACGAAAGTG 745
 |||||
 DB 530 TTGCTCCGCGGCGCTACTTGAAGAAATATTAATTAAGCAAAACGAAAGAACCTA 471
 |||||
 QY 746 TAACAGCGGCTTTCAATTTGGCAATATGACGATACCAAGGCGCAGTGAATACG 805
 |||||
 DB 470 TCACAAATGTGTGTATGTCTTGAACAGTGTCCGATTCGAAATGAGCGGTTATTAAG 411
 |||||
 QY 806 AAGAAAGCAAAATTCATTATACGCAATATACCTCGTATGTGCAACGAACTGAAACT 865
 |||||
 DB 410 AAGTGTGACCTCGATTTACACAAATGTGCGATCATGTGTCGGAAGCAAAACGT 351
 |||||
 QY 866 ACTTTTCCACACTATGACAAATCGCAATCCAAAGTAAATTTATTCATGAAGACC 925
 |||||
 DB 350 ACTATTTTCACTCTACAGAAACCAACCAATCAATAGTTACTTTGTGGAAGAAAGTTA 291
 |||||
 QY 926 TTGACTGTTTGA 938
 |||||
 DB 290 TAGAAATATGCA 278
 |||||

RESULT 2
 C2540175/c 853 bp DNA linear GSS 13-MAY-2005
 LOCUS
 DEFINITION SRA-aad30b09.b1 Strongyloides ratii whole genome shotgun library
 (SRASS 004) Strongyloides ratii genomic, genomic survey sequence.
 C2540175
 VERSION C2540175.1 GI:64664074
 KEYWORDS GSS.

SOURCE Strongyloides ratii
 ORGANISM Strongyloides ratii
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Panagrolaimoidea; Strongyloidea; Strongyloides.

REFERENCE
 1 (bases 1 to 853)
 Miteva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
 Rafter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
 Clifton,S.W. and Wilson,R.

TITLE Genome Survey sequences from the rat parasitic nematode
 Strongyloides ratii
 JOURNAL Unpublished (2005)
 COMMENT Contact: Miteva M

Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@wustl.edu
 Genomic DNA was provided by Fiona Thompson
 (F.Thompson@bristol.ac.uk) and Mark Viney
 (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
 UK.

Class: shotgun.
 Location/Qualifiers
 1..853

FEATURES
 source
 /organism="Strongyloides ratii"
 /mol_type="genomic DNA"
 /strain="isofemale line ED321 heterogenic"
 /db_xref="taxon:34506"
 /dev_stage="infective larval stage (L3)"
 /lab_host="GSI0"
 /clone_lib="Strongyloides ratii whole genome shotgun
 library (SRASS 004)"
 /note="Vector: pOTW13; Site_1: BstXI; Site_2: BstXI;
 Strongyloides ratii genomic DNA was randomly sheared,
 end-repaired and size fractionated to enrich for 2-4 kb

fragments. Genomic DNA was provided by Fiona Thompson
 (F.Thompson@bristol.ac.uk) and Mark Viney
 (Mark.Viney@bristol.ac.uk) at the University of Bristol,
 Bristol, UK. Sequencing by Washington University Genome
 Sequencing Center, St. Louis, MO."

ORIGIN
 Query Match 4.5%; Score 45.2; DB 10; Length 853;
 Best Local Similarity 54.9%; Pred. No. 0.098;
 Matches 89; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 408 GATACAGTTTACCGCTTCACTGATATGTCAGACCGGACCGCAACCTGACGAT 467
 |||||
 DB 257 GAATTTAACTACACATTCACATATGCTTTTATGATTAACACAGGTGTGCAATATGT 198
 |||||
 QY 468 AAGAACAGAGCAGAGCGCTCAAGTCATATGATTAACACCTGATGTCAGCAAG 527
 |||||
 DB 197 TGAAGCGTAAATGCAAAATTAACAGTTTGTATTAACCTACTCGTGTCTATGACTAATGG 138
 |||||
 QY 528 CCCCAGCTTATATGCGATGTAACCAATCTGCAGCAATATAC 569
 |||||
 DB 137 GCCTGATTTTCATGCGATTTTAAACCTGATTAATATAC 96
 |||||

RESULT 3
 CV973894 175 bp mRNA linear EST 01-JAN-2005
 LOCUS
 DEFINITION DDF370 Brassica oleracea DD-PCR fragment Brassica oleracea cDNA 3',
 mRNA sequence.
 CV973894
 VERSION CV973894.1 GI:56957135
 KEYWORDS EST.

SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 1 (bases 1 to 175)
 Casimiro,S., Ze-Ze,L., Tenreiro,R. and Monteirol,A.A.
 Pathogenesis-related cDNA genes isolated by differential-display
 PCR from Brassica oleracea seedlings infected with Peronospora
 parasitica

TITLE Unpublished (2003)
 JOURNAL Contact: Casimiro, S.
 COMMENT Departamento de Biologia Vegetal - Centro de Genetica e Biologia
 Molecular
 Faculdade de Ciencias da Universidade de Lisboa
 Rua Ernesto de Vasconcelos, Ed. C2, Piso 4, 1749-016 Lisboa,
 Portugal
 Fax: +351217500048
 Email: scasimiro@fc.ul.pt

Insert Length: 175 Std Error: 0.00
 Seq primer: T3
 High quality sequence stop: 175
 POLYA=yes.
 Location/Qualifiers
 1..175

FEATURES
 source
 /organism="Brassica oleracea"
 /mol_type="mRNA"
 /culti_vat="CRG3.1", 'Algarvia' and 'Coracao-de-Boi'
 /db_xref="taxon:3712"
 /dev_stage="seven days after infection with Peronospora
 parasitica"
 /clone_lib="Brassica oleracea DD-PCR fragment"

ORIGIN
 Query Match 4.5%; Score 44.6; DB 8; Length 175;
 Best Local Similarity 61.7%; Pred. No. 0.092;
 Matches 71; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 467 TAGAACCAAGCAGACGCGCTCAAGTATGATATCAACCGGTGTCATGACGAACA 526
 |||||
 DB 132 TCGAACCAACGAAAGAAATTAATTTATGATCTCATGCGAGTATGCAAAATA 73
 |||||

QY 527 GCCCCACTTTATATGCGATGTACCAATCTGCAGCAATATACGGAATCAGACC 581
DB 72 GTCTGATTATCTCTGGCATGAATAATTAAGAAATATCTTCAATCAATCAACC 18

RESULT 4
A2533653/c 881 bp DNA linear GSS 03-NOV-2000
LOCUS ENTCS322R Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, genomic survey sequence.
ACCESSION A2533653
VERSION A2533653.1 GI:11089512
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 881)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
JOURNAL Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Classes: shotgun
High quality sequence start: 21
High quality sequence stop: 842.
FEATURES
source location/Qualifiers
1..881
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHD1; Site 1: Bat 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Bartell, Oxford University Press, 1999)."

ORIGIN

Query Match 4.5%; Score 44.6; DB 9; Length 881;
Best Local Similarity 49.8%; Pred. No. 0.15;
Matches 113; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 383 TTGTAGAGAAAAATATAGATCTATTGATGATACAGTTTACCGCTTCAGTGAATTTGTCAG 442
DB 632 TTGTATAGCAAAATATCAACAGTAGAATATCACTTCTGATTTATCATTAATA 573
QY 443 ACCGACGGCGCGGAACCTGACATAGAACCAAGACGACGCGCTCAAGTCTATGATA 502
DB 572 ATCACAATATGTAAGAAACATGACATATTTGGCATATCATATGCGAGAAATTAAGAAA 513
QY 503 ATCAACTGTGTGTCATGACGAACAGCCCGACTTTATATGCGATGATTAACCAATCTGCAGC 562
DB 512 ATACACTGGAATATATCATATTAATAAAACCCCATATGGAACAATGTTCCATATTAAGA 453

QY 563 AATATACAGGAATCAGACCGCAATTAAGAGCAAGAGATGGC 609
DB 452 CATTACAAATGATATTGAAACATCAATATATGATTAAGATGATGAC 406

RESULT 5
A2538681/c 910 bp DNA linear GSS 14-NOV-2000
LOCUS ENTPO66RF Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, genomic survey sequence.
ACCESSION A2538681
VERSION A2538681.1 GI:11143851
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 910)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
JOURNAL Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Classes: shotgun
High quality sequence start: 50
High quality sequence stop: 716.
FEATURES
source location/Qualifiers
1..910
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHD1; Site 1: Bat 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Bartell, Oxford University Press, 1999)."

ORIGIN

Query Match 4.5%; Score 44.6; DB 9; Length 910;
Best Local Similarity 49.8%; Pred. No. 0.15;
Matches 113; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 383 TTGTAGAGAAAAATATAGATCTATTGATGATACAGTTTACCGCTTCAGTGAATTTGTCAG 442
DB 370 TTGTATAGCAAAATATCAACAGTAGAATATCACTTCTGATTTATCATTAATA 311
QY 443 ACCGACGGCGCGGAACCTGACATAGAACCAAGACGACGCGCTCAAGTCTATGATA 502
DB 310 ATCACAATATGTAAGAAACATGACATATTTGGCATATCATATGCGAGAAATTAAGAAA 251
QY 503 ATCAACTGTGTGTCATGACGAACAGCCCGACTTTATATGCGATGATTAACCAATCTGCAGC 562
DB 250 ATACACTGGAATATATCATATTAATAAAACCCCATATGAACAATGTTCCATATTAAGA 191
QY 563 AATATACAGGAATCAGACCGCAATTAAGAGCAAGAGATGGC 609

RESULT 8
A2683787/c
LOCUS A2683787 871 bp DNA linear GSS 14-DEC-2000
DEFINITION ENTX164TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION A2683787
VERSION A2683787.1 GI:11820933
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
REFERENCE 1 (bases 1 to 871)
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HMI:IMSS sheared DNA library
COMMENT Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 25
High quality sequence stop: 860.
Location/Qualifiers
1..871
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

FEATURES

source

ORIGIN

Query Match 4.2%; Score 41.4; DB 9; Length 871;
Best Local Similarity 48.9%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 116;

QY 383 TTGTAGAGAAAATATAGATCTATGTGATACAGTTTACCGCTTCACTGGATTTTCG 442
DB 500 TTGTAAAGACAAATATACACAGTAGACATTTCTATCTTGTATGGCATAAAAA 441
QY 443 ACCGAGCGGGCCGAAACCTGACATAGAACCAAGAGAGAGCGGCTCAAGTCTATGATA 502
DB 440 ATCACAATATGAAAAACATGACCATATAGCATTTATATATGGAGAGTTATATAGAAA 381
QY 503 ATCAACTGTGTGATGACGAGAACGCCCCGACTTTATATGGCATGTAACTCAATCTGACG 562
DB 380 ATATACAGAAATATATCAATATATAAAAACCATATGAAACAGTGTCCCAATATTAAGA 321
QY 563 AATATACAGAAATCAGACCGAGCAATTTAGAGAGCAAGAGATGGG 609
DB 320 CATCAATATATTTTAAACAAATATATGCTATTAAGTATGATGAC 274

RESULT 9
CZ859348/c
LOCUS CZ859348 773 bp DNA linear GSS 27-JUN-2005
DEFINITION OC_Ba0251M04.f OC_Ba Oryza coarctata genomic clone OC_Ba0251M04
5', genomic survey sequence.
ACCESSION CZ859348
VERSION CZ859348.1 GI:71334104
KEYWORDS GSS.
SOURCE Oryza coarctata (Porteresia coarctata)
ORGANISM Oryza coarctata
REFERENCE 1 (bases 1 to 773)
AUTHORS Kim, H., Collura, K., Wisnietki, M., Byrne, M., Stum, D., Smart, D.,
Rao, K., Luo, M., Uetzy, R., Kudrna, D., Muller, C., Soderlund, C. and
Wing, R.
TITLE Oryza Map Alignment Project - Arizona Genomics Institute
JOURNAL Unpublished (2005)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TNG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0251 row: M column: 04
Seq primer: TAA TAC GAC TCA CTA TNG GG
Class: BAC ends.
Location/Qualifiers
1..773
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone_lib="OC_Ba0251M04"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OC_Ba"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

FEATURES

source

ORIGIN

Query Match 4.0%; Score 39.6; DB 10; Length 773;
Best Local Similarity 48.3%; Pred. No. 4.5; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 119;

QY 716 TAGAGCGGGCCGCGATGAAGCAAGAGGTATACAGCCGCTTTCAATTTTGGCAATA 775
DB 230 TAAACACGATTCGTGTGCTGAGCTATCAACCGGGGAGTGTAAAGTGAACCCAAC 171
QY 776 TGAAGTATCCAAAGGCGGAGTATACGGAAGAGCAAAATTCATTATAGCAATATA 835
DB 170 TACTGCAACACAAAGTAAATTAACAGAGTAAAGTTGCACTACTTTATCTGAATAAT 111
QY 836 CTTCGATGATGTCGAACGAACTGGAACCTACTATTTTCCACCACTATGCAATGGCAAA 895
DB 110 GCATATATCTTTCGACTGCAAAAATATTAATTTTATATGCAATTTAGAGATGGCCAAA 51
QY 896 TCCAAAAGTAATTTATTTATTTATGAAAGACTTGACTGTTTGAGGCTTAA 945
DB 50 TGAAGATTAATAAACATGCTCTATATAGAGTTTCAATGCGCAAGATTAAT 1

RESULT 10
CC254220/c
LOCUS CC254220 1055 bp DNA linear GSS 13-MAY-2003
DEFINITION CH261-4N24.Sp6.1 CH261 Gallus gallus genomic clone CH261-4N24,
genomic survey sequence.
ACCESSION CC254220

VERSION CC254220.1 GI:30590970
 KEYWORDS
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1055)
 Krenitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Maritz, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submis@wustl.edu
 Insert Length: 18200 Std Error: 0.00
 Seq primer: SP6 ATTAGGTGACACTATAG
 Class: BAC ends
 High quality sequence start: 113
 High quality sequence stop: 391.
 Location/Qualifiers
 1..1055
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-4N24"
 /sex="Female"
 /cell_line="UCD001, indred 256"
 /clone_11b="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - For library and clone
 ordering information: http://www.chori.org/bacpac"

ORIGIN
 Query Match 4.0%; Score 39.4; DB 9; Length 1055;
 Best Local Similarity 48.4%; Pred. No. 5.6; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 694 GCTGTTATTTGAAAGACATCTAGAGCGGCGCGGTAAGAAAGGTTACAGCC 753
 DB 376 GCCTCCAGTAAAGTGAGCTACTAGACAGTGAACACAGACAGTGCAAAAAGT 317
 QY 754 GCTTTCAATTTTGCAATATGACATACCAAGCGCGCATATACGGAAGAAC 813
 DB 316 GCTGATGAAATCAACGGAATCTTGTATACAAAAGAGTTATGTTAGAGTAAAGCA 257
 QY 814 GAAATTCATTATAGCAATATCTCCGTGATGTGCAAGAACTGAAACTACTATTTC 873
 DB 256 TAAATAGCTAGTTCCTCAATTAAGTTGAAGATACAGACCGTACGAAATTAATTTT 197
 QY 874 CACCACTATGACATCGCAATCCAAAAGTAAATTTATTTTCAT 918
 DB 196 CTTCTACACACAGCAGCGTCACTTCAAGCAATTTTCAAT 152

RESULT 11
 BH059630 512 bp DNA linear GSS 18-JUL-2001
 LOCUS RPCI-24-381C20.TV RPCI-24 Mus musculus genomic clone
 DEFINITION RPCI-24-381C20, genomic survey sequence.
 ACCESSION BH059630
 VERSION BH059630.1 GI:14869888
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 512)
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintun, B., Levins, M.,
 Teagay, G., Geer, K., Kroll, M., Shvartbeyt, A., Gebregeorgis, B.,

TITLE Russell, D., de Jong, P. and Fraser, C.M.
 JOURNAL Mouse BAC End Sequences from Library RPCI-24
 COMMENT Unpublished (1999)
 Other GSSs: RPCI-24-381C20.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 381 row: C column: 20
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..512
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-381C20"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_11b="RPCI-24"
 /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI.
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

ORIGIN
 Query Match 3.9%; Score 38.6; DB 9; Length 512;
 Best Local Similarity 53.7%; Pred. No. 7.8; Indels 0; Gaps 0;
 Matches 80; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 727 GCCGATGAAGAAAGTGTAAGCGCGCTTCAATTTTGGCAATATGACATACCA 786
 DB 103 GCCAACTACTAAAGGCCCGCAGGAGTATCCAAATTTAAATTAAGAAAGCA 162
 QY 787 AAGGCGCAGTATGTAAGCAAGAAAGCAATTCATTATGCAATATCTCCGTATG 846
 DB 163 AAGGAGTTATACACAGAAATGAGAAATTCAAAATATATCAACAACCTGAAAA 222
 QY 847 TGCAACGAACCTGAAACTATATTTC 875
 DB 223 TCTATGATGAATGGAAGTTTCTATACA 251

RESULT 12
 CNS00FOO 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
 DEFINITION BACR31F03 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL070854
 VERSION AL070854.1 GI:4950896
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - web : www.genoscope.cns.fr)

/note="Organ: mammary; Vector: PCMV-SPORE6; Site: 1; Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hemmighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 3.8%; Score 38.2; DB 3; Length 593;
Best Local Similarity 49.3%; Pred. No. 11;
Matches 100; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 721 CCGGCGCCGATGAAACGAGGTGTAAACGCGCTTTTCAATTTTGGCAATATGACG 780
DB 192 CCCCCCCCCCAAAAAAAAAAAAAAAAAACCCCTTTTAAAAAAAAAAAAAAAAACCTT 251
QY 781 ATACCAAGGGCGCGATTAACGAGACGCAATTCATTAATGCAATATATCTCC 840
DB 252 TTTAAAGGGGCAAAAAAAAAATTTGGGGGAAAAAAAAAGGGGGGAAAACTTTGG 311
QY 841 GTGATGTCACGAACTGAAACTACTATTTCCACCACTATGACATCGCAATCCAA 900
DB 312 GAAAAAGAAAAAATTTAAATAATTTTAAATAAATAAATAAAGCTTTTAA. 371
QY 901 AAGTAAATTTATTCATGAAGA 923
DB 372 AAAAAAATTTTAAAAAAA 394

RESULT 15
AZ669903/c 853 bp DNA linear GSS 14-DEC-2000
LOCUS ENTHPI0TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, genomic survey sequence.
ACCESSION AZ669903
VERSION AZ669903.1 GI:11807049
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 853)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
CONTACT: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@igr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: Shotgun
High quality sequence start: 66
High quality sequence stop: 746.
Location/Qualifiers
1..853
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHS01, Site 1; Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,

FEATURES

SOURCE

ORIGIN

Query Match 3.8%; Score 38.2; DB 9; Length 853;
Best Local Similarity 48.0%; Pred. No. 12;
Matches 109; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 383 TTGTAGAGAAAAATAGATCTATTTGATACAGTTTACCGCTTCACTGATATTTGACG 442
DB 525 TTGTAAAGCAAAATATCAACATGAAACATTTCTATCTTTGTATTTGCTATTA 466
QY 443 ACCGAGCGGCGGAACTGACATGAAACCAAGAGAGACGCGCTCAAGTCTATGATA 502
DB 465 ATCAAAATGAAAAACATGACCATATGAGCATTAATATGAGAGGATTAATAGAAA 406
QY 503 ATCAACTGTGTATGACGACGACCCGACCTTATATGCGATGTAAACCATCTGACG 562
DB 405 ATACACTGAAATTAACATATTAATAAACCCTCATATGAAACAGTGTTCATTAAGA 346
QY 563 AATATACGAATGACCGAGCAATTAAGAGCAAGATGAGG 609
DB 345 CATCAATGATATGAAACAAATCATGATTAATGATGAC 299

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Job time : 4770 secs

H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:46:58 ; Search time 226 Seconds
(without alignments)
7833.856 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996
Sequence: 1 catatgtgcacaaagcttacc.....atgagcttaataagatcc 996

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
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8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	16.0	990	US-09-710-279-413	Sequence 413, App
2	159	16.0	996	US-09-134-001C-2421	Sequence 2421, Ap
3	159	16.0	2975	US-09-710-279-3345	Sequence 3345, Ap
4	159	16.0	4114	US-09-710-279-4184	Sequence 4184, Ap
5	146	14.7	11466	US-08-956-171E-444	Sequence 444, App
6	146	14.7	11466	US-08-781-986A-444	Sequence 444, App
7	95.4	9.6	987	US-09-134-000C-838	Sequence 838, App
8	82.6	8.3	978	US-09-107-532A-366	Sequence 366, App
9	47.8	4.8	400	US-08-956-171E-3720	Sequence 3720, Ap
10	47.8	4.8	400	US-08-781-986A-3720	Sequence 3720, Ap
11	39	3.9	7218	US-08-232-463-14	Sequence 14, Appl
12	37.4	3.8	10714	US-09-949-016-14834	Sequence 14834, A
13	36.4	3.7	61663	US-09-453-702B-62	Sequence 62, Appl
14	36.4	3.7	61663	US-10-114-170-62	Sequence 62, Appl
15	34.4	3.5	4429	US-09-455-486-7	Sequence 7, Appl
16	34.2	3.4	2067	US-09-106-194-11	Sequence 11, Appl
17	34	3.4	505	US-09-621-876-15639	Sequence 15639, A
18	34	3.4	1083	US-09-134-000C-2381	Sequence 2381, Ap
19	33.4	3.4	825	US-09-313-294A-5605	Sequence 5605, Ap
20	33.2	3.3	2228	US-09-270-767-25560	Sequence 25560, A
21	33.2	3.3	2228	US-09-270-767-10203	Sequence 10203, A
22	33.2	3.3	2460	US-08-952-165-1	Sequence 1, Appl
23	33.2	3.3	6065	US-09-800-729-35	Sequence 35, Appl
24	33.2	3.3	101011	US-09-949-016-16933	Sequence 16933, A

C 25	33	3.3	1801	3	US-08-669-304-30	Sequence 30, Appl
C 26	33	3.3	1801	3	US-09-824-053-30	Sequence 30, Appl
C 27	33	3.3	247299	3	US-09-949-016-17590	Sequence 17590, A
C 28	32.6	3.3	1200	3	US-09-107-532A-19	Sequence 19, Appl
C 29	32.6	3.3	1509	3	US-09-248-796A-3224	Sequence 3224, Ap
C 30	32.4	3.3	601	3	US-09-949-016-113423	Sequence 113423, A
C 31	32.4	3.3	601	3	US-09-949-016-163399	Sequence 163399, A
C 32	32.4	3.3	601	3	US-09-949-016-163400	Sequence 163400, A
C 33	32.4	3.3	601	3	US-09-949-016-163401	Sequence 163401, A
C 34	32.4	3.3	1340	3	US-08-956-171E-245	Sequence 245, App
C 35	32.4	3.3	1340	3	US-08-781-986A-245	Sequence 245, App
C 36	32.4	3.3	85869	3	US-09-949-016-12017	Sequence 12017, A
C 37	32.4	3.3	85878	3	US-09-949-016-16321	Sequence 16321, A
C 38	32.4	3.3	167708	3	US-09-949-016-16423	Sequence 16423, A
C 39	32.4	3.3	285966	3	US-09-949-016-12287	Sequence 12287, A
C 40	32.4	3.3	288031	3	US-09-949-016-14864	Sequence 14864, A
C 41	32.2	3.2	832	3	US-09-621-876-2813	Sequence 2813, Ap
C 42	32.2	3.2	255679	3	US-09-949-016-17189	Sequence 17189, A
C 43	32.2	3.2	786431	3	US-09-751-389-3	Sequence 3, Appl
C 44	32	3.2	870	3	US-09-543-681A-3984	Sequence 3984, Ap
C 45	32	3.2	930	4	US-09-605-703B-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-710-279-413
Sequence 413, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/09/710, 279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164, 258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 413
LENGTH: 990
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-09-710-279-413

Query Match 16.0%; Score 159; DB 3; Length 990;
Best Local Similarity 49.8%; Pred. No. 1.4e-39;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
QY 2 ATATGTGACAAAGCTTACATTTGAAAGCTGACCGTAACATGATTAGCAAGAACAA 61
DB 8 ATATGTGACCTGACATTTCTTATATATACAAACAGTTACATTTATTAGTAGAACA 67
QY 62 TGGATTTTTCATTTTACGCTGGGAGACAGAGTATTTCTATCCGCCCGTTACAGTGA 121
DB 68 TGGATTTTTCATTTTGAATTTAATGTATCCCAACATTTTCCACGCCATTTACCTACC 127
QY 122 ACAGTGAAGCTACAGGAGGCCCATACAGACAGTACCGTTATTCGGATGAGGAGAA 181
DB 128 AATTGATGATTAATTCAGACATGCGCTT---GAATATGTTTGTGGAACAATTAA 184
QY 182 AACTTGAAATATATTTATTTGCGACGCGATTATGAAGCGGTTATCTTGTGCGCGC 241
DB 185 AAGTGAAGAGTATGATTTGATGTGATGATTAACCAAAAGGTTAGCTATTTGCAAC 244
QY 242 TTTATTTTCCGGCGATGCGAGTACGAAACATATAGGAGATACCGTTACATG 301
DB 245 ATTACTTACTGTGTAAGCTTCATCAAGTACCATTAACGTTATGTTAATTTAACTTAG 304

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14  ATATGTGACAGCCATTCTTTATATACAAAGCAAGTACCATTAATTAGTAGAACA  73
QY      62  TGGATTTTGCATTTACGCTGGGGACAGAGGTATCTCTATCCGGCCCGTTACAGTTGA  121
Db      74  TGGACTTTGCATTTGAATTTAATGAGTATCCCAACCATGTTTCAAGCCATTTACCTACC  133
QY      122  ACAGTGAAGCTGACGGAAGGGCCCATCAGACACAGTACGCGTTTATCGGTATGGGAGAA  181
Db      134  AATTGATCTGATTCACAGCATGCCTTT---GAATAGTTTTGTTGGAACAAATTTAA  190
QY      182  AACTTGGAAATATATATTTTGGCCGACGCGCATTAATGAAGCGGTTATCTTGTGGCGCG  241
Db      191  AAGTGAAGCGTTATGATTTGGTGTGATGAAGAAAGAAAGTTTGAAGTTATTTCAAAC  250
QY      242  TTTATTTCCGGGGCTATGCGGAGTACGAAAGAAACATACGCGAAGATACCGTTACATTS  301
Db      251  ATTAATTCTACGTGTGAAGGCTCATACAGTACCCATTAAGGTTATGTTATTTTAATTAG  310
QY      302  TCCCGCATGATTTGTGACATGGGTGCTGTCACTGTCTAGTCTTTTGAAGACGTAAAG  361
Db      311  CACCTGAAGAGTTTATGTTTGGGTTTAAAGTTTAAATGAAGTATTAACGATTTAAAC  370
QY      362  AAAAGATTCGATCTTTAAGATGTGAGAAATAATAGATCTATTTGATACAGTTTAC  421
Db      371  AAAAGGTGAAGAAATCAATATTAATGAATGAAGAAATAATTCGACTTGAATATGTTCTC  430
QY      422  CGCTTCACTGTATTTGTCAAGCCGAGCGGCGCAACCTGACGATAGAACCAAGACAG  481
Db      431  CTTTACATTTCAATGCTCACTGATGAAGACAGCATACGTTAGCATAGAACCTCACAATG  490
QY      482  ACGGCTTCAAAAGTCTATGATTAATCAACTGTTGTCTATGACGAAACAGCCCGACTTAT  541
Db      491  GCTTATATATGTTTAAAGATATTTATTTGTTCATACCTTAAACAAATGAACCTTAATTA  550
QY      542  GGCATGTATACCAATCTGACGACAAATATACAGAAATCAGACCAAGCAATTAAGAGCAAG  601
Db      551  GGCAATCTATCTTACTTAAGAAATTAACGCTTTTAAAGCCACAGAAATCAACCAATCAAT  610
QY      602  AGATGGGCGATTTAGCCCTTTCTGCTTTTGGCCAAAGCTTAGAACTGTTGGTCTGCGG  661
Db      611  TAAATGTGTAAGTGTATGATAGATCAATGGGCTGTGAAGACAGAACAAATGGCTTTACGG  670
QY      662  GGGATTAATACACCGGCTTCCGGTTTGTACAGAGCTGTTATTTGAAAGACATCTAGAGC  721
Db      671  GTGTTATATACGTCACACAGATCGTTTATATACGGCTACATATTTAAGACACCAACTACGCT  730
QY      722  CGGCGCGCGATGAAGACGAAGGTGTACAGCCGCTTTCAAAATTTGGCAAAATATAGCGA  781
Db      731  GTTCCCATATGAAGATGAAGAAATTTAATGAATTTGTTTAAAGTTCTAGATCAGTCAATA  790
QY      782  TACCAAGGGCGGCAATGATTAACGGAAGAAAGCAAGAAATTCATTTATCGCAATATACCTCG  841
Db      791  TCCCTCAAGGTGCAATTAAT--CGATGCCAATAAATATATTAACACACAAATCAATTAAG  847
QY      842  TGAATGCAACGAATCTGAACACTATATTTCCACACACTATAGCAATCGGCAAAATCCAA  901
Db      848  TGAATGAAGTAAGTAAGAAAGAACTTATTTATTAATTAAGCTTAAGCTTAACATCAAAATTTCA  907
QY      902  AAGTAATTTATTTCAATGA  920
Db      908  AAATAAATTAACATGAAGA  926

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; RESULT 3
; US-09-710-279-3345/C
; Sequence 3345, Application US/09710279
; Patent No. 6703492
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; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09

```

PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3345
LENGTH: 2975
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3345

Query Match 16.0%; Score 159; DB 3; Length 2975;
Best Local Similarity 49.8%; Pred. No. 2.5e-39;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTGCAAGCTTCTTACATTTGGAACTGCTGACCTTAACATGTATTGCAAGAACAA 61
DB 1755 ATATGTGCTGCTCCATTTCTTTATATACAAACACCTTACATTTATTTAGCTAGAACAA 1696
QY 62 TGGATTTTGCATTTGAGCTGGGACAGAGGTGATTCCTATCCGCGCCGTTACAGCTGGA 121
DB 1695 TGGACTTTGATTTGATTTAATGATATCCCAACCATTTGTCACGCCATTATCATCTACC 1636
QY 122 ACAGTAAGCTGACGGAAGGCCCATCAGACAGTACGGGTTATCGGTATGGGAGAA 181
DB 1635 AATTGATCTAGATTCAGATCATGCGTCTT--GAATATGTTTGTGGAAACAATTTAA 1579
QY 182 AACTTGAATAATATTTATTTGCGAGCGCATTAATGAAACGGTTATCTTGCGCGCG 241
DB 1578 AAGTAGAGCTTATGATTTGATGATGATTAACGAAAGGTTTATGATTTTCAACC 1519
QY 242 TTTATTTCCGGGCTATGCGAGTACGAAACAAACATGCGGAGATACCGTTACATTTG 301
DB 1518 ATTACTTCACTGCTGAGAGCTCATACGATCCATTAACGTTATGTTATTTTAACTTAA 1459
QY 302 TCCCGCATAGTTTGAACATGGGCTGTCACTGTGTCAGTCTTTGGAAGAGTAAAG 361
DB 1458 CACTGAGAGTTATTTGTTGGTTTAAAGTTTAAAGATTAAGGATTAAG 1399
QY 362 AAAAGTTGATTTTAAAGATTTGATGAGAAATTAATGATCTATTGATCACTTTTAC 421
DB 1398 AAAAGTTGAGAAATCAATTTATGATGATGAAATTAACGATTTGATGTTCTTC 1339
QY 422 CCGTCACTGATATTTGTCAGACGCGAGCGGCGAAACCTGACATAGAACCAAGACG 481
DB 1338 CTTTACATTTTCACTGATGATGAAACGAGATACCGGACATAGAACCTTCACATG 1279
QY 482 ACGGCTCAAGTCTATGATTAATCAACTGTGTGTCATGACGAAACAGCCCGCATTTAT 541
DB 1278 GCTTATTAATAGTTAAAGATTAATTTAGTTTATACCTTAACAAATGAACCTTAAT 1219
QY 542 GGCATTTAACAATCTGACAGCAATATACAGAAATCAAGCCGAAATTAAGAGCAAG 601
DB 1218 GGCATTTAACAATCTTAAAGAAATTAAGCTTTTAAAGCCACAGAAATTAACCAAT 1159
QY 602 AGATGGGCGATTAAGCCCTTTCGCTTTTGGCCAAAGGCTTAAAGCTGTTGGTCCGG 661
DB 1158 TAAATAGTAAAGTCTAGTAAATCAATGAGGCTGTAAGAGGAAATAGGCTTAACGG 1099
QY 662 GGGATTTATACACGCTTCCCGGTTTGTGAGAGCTGTTTATTTGAAGAACTTACAG 721
DB 1098 GTGGTTATACGTCACAGATCGTTTAAACGGCTACATATTTTAAACACCACTACG 1039
QY 722 CGGCGGCGCATGAAAGGAGTAAAGGCTTTTCAATTTTGGCAATATGACGA 781
DB 1038 GTTCCATATATGAAAGTAAATTTATGATTTTAAAGTTCTAGATCACTACGTA 979
QY 782 TACCAAGGCGCATGATTAAGAGAAAGCAAAATTTATTAAGCAATATTAATCTTCCG 841
DB 978 TCCCTCAGGTGCACTTAT--CGATGCCAATTAATTAACATTAACACAAATTCATTTAG 922

QY 842 TGATGTGCAAGAACTGGAACCTACTATTTCCACCATATGACAAATCGGCAATCCAA 901
DB 921 TGATGAAAGTAAAGAAAGATTTATTTAAGCTTAACTTAAATCAATTTTCA 862
QY 902 AAGTAAATTTATTTCTATGA 920
DB 861 AATTAATTAATTAAGTGAAGA 843

RESULT 4
US-09-710-279-4184
Sequence 4184, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P0348005
CURRENT APPLICATION NUMBER: US/09/710,279
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4184
LENGTH: 4114
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4184

Query Match 16.0%; Score 159; DB 3; Length 4114;
Best Local Similarity 49.8%; Pred. No. 2.9e-39;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTGCAAGCTTCTTACATTTGGAACTGCTGACCTTAACATGTATTAGCAAGAACAA 61
DB 1626 ATATGTGCTGCTCCATTTCTTTATATACAAACAGTTACATTTATTTAGTAGAACAA 1685
QY 62 TGGATTTTGCATTTGAGCTGGGACAGAGGTGATTCCTATCCGCGCGTTACAGCTGGA 121
DB 1686 TGGACTTTGATTTGATTTAATGATATCCCAACCATTTGTCACGCCATTATCATCTACC 1745
QY 122 ACAGTAAGCTGACGGAAGGCCCATCAGACAGTACGGGTTATCGGTATGGGAGAA 181
DB 1746 AATTGATCTAGATTCAGATCATGCGTCTT--GAATATGTTTGTGGAAACAATTTAA 1802
QY 182 AACTTGAATAATATTTATTTGCGGACGCTTAATGAAACGGTTATCTTGCGCGCG 241
DB 1803 AAGTAGAGCTTATGATTTTGTGATGATTAAGAAAGGTTTATGATTTTGAAC 1862
QY 242 TTTATTTCCGGGCTATGCGGAGTACGAAACAAACATACGGAAGATACCTTACATTTG 301
DB 1863 AATTCTTCACTGCTGTAAGCTCATACAGTACCATTAACGTTATGTTTAACTTAA 1922
QY 302 TCCCGCATAGTTTGAACATGGGCTGTGTCAGTCTGTCAGCTTTGGAAGCGTAAAG 361
DB 1922 CACTGAGAGTTTATGTTTGGGTTTAAAGTTTAAATTAAGTTTAAAGCAATTTAAAC 1982
QY 362 AAAAGTTGATTTTAAAGATTTGATGAGAAATTAAGATCTATTTGATCACTTTTAC 421
DB 1983 AAAAGTTTAAAGAAATCAATTTATGATTAAGAAATTAAGCACTTTGAATATCGTTCTTC 2042
QY 422 CCGTCACTGATATTTGTCAGACGCGGCGGAAACCTGACATTAAGAACCAAGACG 481
DB 2043 CTTTACATTTTCAATGCTGATGAAACAGACATACCGTACCTATGAACTTCACATG 2102
QY 482 ACGGCTCAAGTCTATGATATCAACTGTGTGATGACGAAACAGCCCGCATTTATAT 541
DB 2103 GCTTATTAATAGTTTAAAGATTAATTTGTTCACTTAAACAAATGAACCTTAATTTAGAT 2162
QY 542 GGCATGTAAACAATCTGACGAAATATACAGAAATCAAGCCGAAAGATTTAGAGCAAG 601

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Db      2163  GGCATCTATCTAAGTAAGAAATACGCTTTTAAAGCCACAGAAATCAACCATCAAT 2222
Qy      602  AGATGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTAGAACTGTGTGTCGCG 661
Db      2223  TAATAGTAAGTCTAGTAAGATCAATGAGCTGTGAAGCAAGAAATGGCTTACCG 2282
Qy      662  GGGATTTACACCGCTTCCGCTTGTGACAGCTGTTTATTTGAAAGAACATCTAGAG 721
Db      2283  GTGGTTATAGTCAACAGATCGTTTATAGCGCTACATTTTAAGACCAATAGCGT 2342
Qy      722  CGGCGCCGATGAACGAAAGGTGAACAGCCGCTTTCAATTTGGCAATATGACGA 781
Db      2343  GTTCCCATTAATGAAGATGAATTAATGAATGTTTAAAGTCTAGAACTCACTGATA 2402
Qy      782  TACCAAGGCGCGATTAACGAGAAAGCAATTCATTAAGCAATATCACTCCG 841
Db      2403  TCCCTCAAGGTGCGATTAT--CGATGCAATTAATAATCAATTAACATCAATAG 2459
Qy      842  TGAATGCAACGAAGTGAAGTACTATTTCCACCACTATGACATCGGCAATCCAAA 901
Db      2460  TGAATGAAGTAAGAAAGAAAGTATTTATTTAAGCCTTACTTAGCATCAATTTTCA 2519
Qy      902  AAGTAATTTATTTTCATGA 920
Db      2520  AATTAATTTAATGAAGA 2538

```

RESULT 5
US-08-956-171E-444/c
Sequence 444, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5236

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 1146 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 444:
US-08-956-171E-444

Query Match 14.7%; Score 146; DB 3; Length 11466;
Best Local Similarity 47.5%; Pred. No. 6,3e-35;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

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Qy      4  ATGTCACAAAGTCTTACATGTGAAGAACTGCTGACCGTAAACATGTATTTAGCAAGCAATG 63
Db      3688  ATGTGACAGAGATTCACATACAACTTTAAATATCAAGTACTTCTTGGACGACATG 3629
Qy      64  GATTTTCATTTGACGTGGGACAGAGTGATTTCTATCGCGCGCTTAAGCTGAAC 123
Db      3628  GATTATGATTTATCATTTAAGTGTGCGCAGCATGACGCTGAATATTCGTTGAAA 3569
Qy      124  AGTGAAGCTGACGGAAGGCCCATCAGACACATGAGCGTTTATGCGTATGGGAGAAA 183
Db      3568  TCTTGCACCT--GGACAGACAGGCCAAACGCAATATGCTTTATGCGACAGAAACGAT 3512
Qy      184  CTGGAATATATATTTATTTGCGACGCGCATTAATGAAGCGTTTATCTTGCGCGCTT 243
Db      3511  ATGGAAGCTTTATTTATGTGATGTGTTAATGAACATGCGCTTGCATTGAACACA 3452
Qy      244  TATTTTCGGGCTATGCGGAGTAAGAAAAAGATACGGAAGATACCGTTACATTGTC 303
Db      3451  TATTTCCGAGGTATATGTTATCATATGATCAACACACAAAGCGGACGATGAATATACG 3392
Qy      304  CCGCATGATTTGTGACATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
Db      3391  CAATAAGTAATGTGACATGATGATTTGGGATATACAAAGCATTTGAAGATGAAACAA 3332
Qy      364  AAGATTCATCTTAAACATTTGATGAAGAAATTAAGATCTATTTGATATGATTTTACG 423
Db      3331  CAGACATCCCAATATCATGTGTAGCTGTATATTTAATGACATCGGTGAAGTCCGCCA 3272
Qy      424  CTTCATCTGATATTTGTCAGACCGGACCGGCGGAACTGACGATAGAACCAAGACGAC 483
Db      3271  TTGCATATCATGTTTCCGATGCAACTGACATACAGTCCAGATTTCAATTAAGAGGGT 3212
Qy      484  GGCTCAAGTCTATGATTAATCAACCTGTGTGATGACGAAAGCCCGCTTATATGG 543
Db      3211  GAAATGTTTAAAGATTAATCTATTTGTTGCTTAAACAATCATCCAGACTTAAATGG 3152
Qy      544  CATGTACCAATCTGACGACATATATACGATACGACCGAAGCAATTTAGAGAGCAAG 603
Db      3151  CATATATGTAATTTAAGACATATATATCAATTTCTCTTATCCAGACACAGCAATTTA 3092
Qy      604  ATGGCGGATTAAGCCCTTCTGCTTTTGGCCAAAGCTTAGAACTGTGCTGCGGGG 663
Db      3091  TTGGAAGGTGTAACGATTTGAACCTTTAGGCAATGAAACAGGTACATTTGGAATCCAGGT 3032
Qy      664  GATTATACACCGCTTCCGCTTGTGTCAGAGCTGTTATTTGAAGAAACATCTAGAGCG 723
Db      3031  GGATTTACTTCAACTGAGCGCTTTGTGAATGCAATTTAAGAAAGCAACATGCTCAA 2972
Qy      724  GCGGCGGATTAAGCAAGAGGTGTAACAGCGCTTTTCAAAATTTTGGCAATATGACATA 783
Db      2971  AACATATATTAAGAAAGATTTAATGATGATGATTTATTTATTAAGATGGGTAAATTA 2912
Qy      784  CCAAGGGCGCAGTGAATACGGAAGAAAGCAAAATTCATTAACGCAATATATCTTCCGTG 843
Db      2911  CCGATGGAATTTGATCGTCGCAATGATGATGATGATGATGATGATGATGATGATGAT 2852
Qy      844  ATGTCACGAAACTGGAATCTATTTCCACATATGACATTCGCAATTCGCAATTCGCAAAA 903
Db      2851  ATTAATTTAATCAAGAAAGTATATTAATTAATTAATTAATTAATTAATTAATTAATTA 2792
Qy      904  GTAATTTATTTCAATGAAGCTTGAAGCTTTGAGGCTTAAGTGTGTTCCGCTTAAGCA 963
Db      2791  TTAAAGCTCACAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2732

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QY 964 GAAGAGTATTCATGAGCTTAATTA 989
DB 2731 CATATCACTATTAGAAAGTTGAATGA 2706

RESULT 6

US-08-781-986A-444/C
Sequence 444, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 11466 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-444

Query Match 14.7%; Score 146; DB 3; Length 11466;
Best Local Similarity 47.5%; Pred. No. 6.3e-35;

Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

QY 4 ATGTGCAAGTCTTACATGGAACCTGACCGTAACATGATTAAGCAACAATG 63
DB 3688 ATGTGCAAGTCTTACATGGAACCTTAAATCACTACTTCTTGACGACGATG 3629
QY 64 GATTTCGATTCAGCTGCGGACAGAGGTGATCTTATCCGCGCTTACACTGGAAC 123
DB 3628 GATTTCGATTCAGTATGATGATGCTGCGACAGTACGCTGAATATGCTTGAAA 3569
QY 124 AGTGAAGCTGACGGAAGGCGCCATCAGACACATGACCGTTATTCGTATGGGAGAAA 183
DB 3568 TCTTGACCT--GGCAGCAGAGGCGCAACGCAATATGCTTTATTTGGCAGAGAAAGAT 3512
QY 184 CTGGAATATATATTTATTTGCGACGACATTAATGAAGCGTTATCTGTGCGGCGCTT 243
DB 3511 ATGGAAGTATATTTATTTATGATGATGATGATTAATGAACATGCGCTTGCATTTGAACAA 3452
QY 244 TATTTTCGGGCTATCGGAGTACGAAAAACATACGGGAGATACCGTTCACTTGTG 303
DB 3451 TATTTTCGGGCTATCGGAGTATGATGATCAACACACAAACGCGACGATGATTAATGACG 3392
QY 304 CCGCATGATTTGTGACATGCGGTGCTGTGCTGTGCTGCTGCTTGAAGACGTAAGAA 363

DB 3391 CAAATGAAATTTGACATGATTTTGGATATACAAAGCATTTGAAGATATGAACAA 3332
QY 364 AAGATTCATCTTTAAGATTTAGAGAAAAATTAATGATCATATGATGATGATTTACCG 423
DB 3331 CAAAGATCCCAATATACATGTTGTAGCTGTATATTTAATGATCGGTGAAGTTCCGCA 3272
QY 424 CTTCATGATATATTTGACAGCGGACGCGGCAAACTGATGATGAACCAAGACAGAC 483
DB 3271 TTGCATATATCATGTTTCCGATGCACTGACATATACATGATGATGATTTAAGAGGGT 3212
QY 484 GGCTCAATCTATATATATCAACTGTGTATGACGAAACAGCCCGCATTTATATG 543
DB 3211 GAAGTGTATTAAGATATCTTATGTTGTGCTTTAACAATCATCAAGCTTAAATTTG 3152
QY 544 CATGTAACATCTGACGATATATACAGAAATGACGCAAGCAATTTAGAGAGAGAG 603
DB 3151 CATTTATATATTTAAGATATATATATATATTTCTTATCAGACAGCAATTTTA 3092
QY 604 ATGGCGGATTAAGCCCTTCTGCTTTTGGCCAAAGGCTTGAAGACTGTGTGCTGCGGG 663
DB 3091 TTGGAAGGTATACATGATGAACCTTATGCAATGAAGACAGGTACATTTGATTTCCAGGT 3032
QY 664 GATTATACAGCGCTTCCGCTTTGTCAGAGCTGTTATTTGAAGAACATCTAGACCG 723
DB 3031 GAATTAATCTTCACTGAGCGCTTTGAGATGCAATTTAAGAAAGCAATTTGCTCAA 2972
QY 724 GCGGCGATGAAGCAAGGATGACAGCGCTTTTCAATTTTGGCAATTTATGACATA 783
DB 2971 AACATATATTAAGAAATGATTTAATGATGATGATTTATTTATGATGCGGTAAATTA 2912
QY 784 CCAAGGCGGACATGATTAACGGAAGAACGAAATTCATTAACGAAATATCTCCGTG 843
DB 2911 CCGATTTGAATTTGATGCTCGCATGATGCTGACATACATCATATGATGATGACAGCTA 2852
QY 844 ATGTGCAAGAACTGGAACCTACTTTTCCACCATATGACATGCGCAATCCAAAA 903
DB 2851 ATTAATTTAATTAAGAAAGCTTATATTAATTAATTAATGAGCAATGATTAAGTGA 2792
QY 904 GTAATTTATTTATGATGACCTTGAAGCTTTGAGACCTTAAGTGTGTTCCGCTAAAGCA 963
DB 2791 TTAAAGCTCAGATATATTTAATTAATTAAGAAAGATGATGATTTTAAGCTGAGAG 2732
QY 964 GAAGAGATTTATCATGAGCTTAATTA 989
DB 2731 CATATCACTATTAGAAAGTTGAATGA 2706

RESULT 7

US-09-134-000C-838

Sequence 838, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 838

LENGTH: 987

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-838

Query Match 9.6%; Score 95.4; DB 3; Length 987;

Best Local Similarity 45.8%; Pred. No. 1.6e-19;

Matches 407; Conservative 0; Mismatches 476; Indels 6; Gaps 2;
QY 41 AACATGATATGCAAGAACATGATTTTGCATTTCAAGTGGGACAGAGGTGATTTCT 100

Db 605 GTTGAATGCTTAAGCCGCGTATGAGGAGATAGGCTTCCCTGGAATTTATCTTCAAG 664
QY 677 CTTCGCCGTTTGTGAGAGCTGTTTATTTGAAGAATCATCTAGAGCCGCGCCGATGAAA 736
Db 665 TATCTCGTTTGTAAAGCGACTTTTACGAGAGCTGAATCTGTATCTGAGATTCAGAGT 724
QY 737 CGAAAGGTGACAGCCGCTTTTCAATTTGGCAATATGACATACCAAGGCGCAG 796
Db 725 CAGAAATATATAGTCAATTTTCCATATCTTAGTTCAGTGAACAACAAGAAAGTTTGT 784
QY 797 TGATACGGAAGAGAGCAATATGATTAAGCAATTAATCTCCGTATGCAACAAA 856
Db 785 GTGATGTTGGTGAAGAAATATGAAATATACAAATTTATCTTGTTCAGATGTCACA 844
QY 857 CTGGAATCTATATTTCCACCATATGACATCGGCAATCCAAAGTAATTTATTTTC 916
Db 845 AAGGAATCTATTAATTCAGAACATATGAGACATCAATTAATGCAATTCATATGATA 904
QY 917 ATGAAGCTTGACTGTTTGGAGCCCTAAAGTGTTCGCTAAAGCAGAGAGATATTC 976
Db 905 AAGAAAGCTTAGATAGTATGATTAATAGTATCAATATAGAAACAAACAATTA 964
QY 977 ATGAGCTTAATTA 989
Db 965 AATATATTAATTA 977

RESULT 9

US-08-956-171E-3720/c
Sequence 3720, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
US-08-956-171E-3720

Query Match 4.8%; Score 47.8; DB 3; Length 400;
Best Local Similarity 48.1%; Pred. No. 0.0001;
Matches 136; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 286 GATACCGTCACTTTCGCCGATGATTGTGACATGAGGTGCTGATGTCAGTCT 345
Db 333 GAGCCATGATATTTACGCAAAATGAATTTGACATGATTTTGGATTTACACAAGC 274
QY 346 TTGAAAGACCTAAAGAAAGATTCATCTTAACGATTTAGAGAAAATTAATGATCTA 405
Db 273 ATGGAAGATATGAAACAACAAGCATCCAAATACATGTTGTACTGTATTAATGAC 214
QY 406 TTGATACATTTTACCGCTTCACTGGATATTGTGACAGCCGAGCGCAAACTGACG 465
Db 213 ATCGTGAAGTTCGCCCATTTGATATCATGTTTCCGATGCACTGACATACAGTCGAA 154
QY 466 ATGAACAAGAGACAGCGCCTCAAGTATGATATGACCTGCTGTCATGACGAC 525
Db 153 GTTCAATTTAAAGAGGTGAAGTGTATTAAGATTAATCTATGTTGTCTTAACAAT 94
QY 526 AGCCCGACTTTATATGATGATGATTAACCAATCTGCAGCAATATA 568
Db 93 CATCCAGACTTAATTTGGATTTATGTAATTTAAGCAATATA 51

RESULT 10

US-08-781-986A-3720/c
Sequence 3720, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-781-986A-3720

Query Match 4.8%; Score 47.8; DB 3; Length 400;

Best Local Similarity 48.1%; Pred. No. 0.0001;
Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 286 GATACCGTTCATGTCCTCCGATGAGTTGTGACATGGGTGCTGACGTCTCT 345
Db 333 GACCGCATGATATATTACGCAAAATGAAATGTGACATGATTTGGGATATACAAAGC 274
QY 346 TTGGAACACCTTAAGAAAAGATTCGATCTTTAAGATTGAGAAAATTTGATCTA 405
Db 273 ATGGAATATGAAACAAACGATCCCAATATACATGTTGATGATTTAAATGAC 214
QY 406 TTGGATACAGTTTACCGCTTCACTGATATTGTCAACCGAGCGCCGAACCTGACG 465
Db 213 ATCGGTGAAGTTCGCCATTCATTCATGTTCCGATGCACTGGACATACAGTGA 154
QY 466 ATGAAACCAAGACGACGCGCTCAAAAGTCTATGATATCACTGGTGTATACGAC 525
Db 153 GTTTCATTAAAGAGGGTGAAGTGTATATAAAGATATCTTATGTTGTTTAACAAT 94
QY 526 AGCCCGACTTTATAGCATGTATACCAATCTGACAGCAATATA 568
Db 93 CATCGACCTTAATTTGGCATTAATGTAATTTAAGACATATA 51

RESULT 11

US-08-232-463-14/c
Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOULPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: PTZpT-F15

US-08-232-463-14

Query Match 3.8%; Score 39; DB 2; Length 7218;
Best Local Similarity 5.8%; Pred. No. 0.28;
Matches 24; Conservative 206; Mismatches 181; Indels 0; Gaps 0;

QY 458 ACTGACATGAAACCAAGACGAGCGCTCAAACTATGATATCAACCTGGTGTCA 517
Db 1436 ACRR 1377
QY 518 TGACGACAGCCCGACTTATATGATGATACCAATCTGACGATATACAGATCA 577
Db 1376 RRR 1317
QY 578 GACCGAAGATTGAGAGACGAGATGCGGATTAAGCTTTGCTTTGGCCAAG 637
Db 1316 RRR 1257
QY 638 GCTTAGAAGTGTGCTGCGCGGAGATTATACCGCTTCCGGTTGTGACAGCTG 697
Db 1256 RRR 1197
QY 698 TTATATTGAAAGACATCTAGACCGCGCGATGAAAGAAAGGTGTACAGCGCTT 757
Db 1196 RRR 1137
QY 758 TTCAAAATTTGGCAATATGACGATACCAAGGCGCATGATTAACGAAAGACAAA 817
Db 1136 RRR 1077
QY 818 TTCAATATACGCAATATATCTCCGTGATGCAAGAACTGGAATCTACT 868
Db 1076 RRRRRRRRRATGCAAGCTCCTCGACCTGCAAGCAAGCTCGAATTAAT 1026

RESULT 12

US-09-949-016-14834

Sequence 14834, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14834

LENGTH: 107140

TYPE: DNA

ORGANISM: Human

US-09-949-016-14834

Query Match 3.8%; Score 37.4; DB 3; Length 107140;
Best Local Similarity 49.7%; Pred. No. 3.7;
Matches 95; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 682 CGTTTGTACAGAGCTGTTTATTTGAAAGACATCTAGAGCCGCGCGATGAACGAAA 741
Db 3534 CGTTTGGAGAGGTGTATTTTAAABAAAAGGACAGAGCGCATTTTAAAGAAAAA 3593
QY 742 GGTGTACAGCGCTTTTCAATTTTGGCAATATGACGATACCAAGGCGCGATGTA 801
Db 3594 AGGAAACAGAGGATGTTTCTGTGTGAGGATGACCAAGAAAGCCTGTGGGTCTTT 3653
QY 802 ACGGAAGAGAGCAATTCATTATACCAATATCTCCGATGATGTGCAAGAACTGGA 861
Db 3654 GCCATAGCACTTACCTTTTAAACGAAAACATCCCATTAACATGATTTTGT 3713


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RESULT 15
US-09-455-486-7/c
; Sequence 7, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-11
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (85)...(1464)
; US-09-455-486-7

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Query Match	Score	DB	Length
3.5%	34.4	3	4429

Matches	80;	Conservative	0;	Mismatches	76;	Indels	0;	Gaps	0;
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QY 243 TTATTTTCCGGCTATTCGGAGATACGAAAAACGATAGCGGAAGATACCGTTCACATTGT 302

Db 1726 TCAATCTCAGCTCCATGCGCTCTGGGAAAATATGAGTCAGGGACCTGCATATTCTTCA 1667

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QY 363 AAAGATTCGATCTTTAAGATTGTGAGAAAAAT 398

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Search completed: March 18, 2006, 11:58:33
Job time : 228 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:52:29 ; Search time 992 Seconds
(without alignments)
8302.722 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996 1 catatgtgcacaaagctctac.....atgagcttaataagatcc 996

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_NA_Main:
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10: /cgn2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	996	9 US-10-812-387-1	Sequence 1, Appl1
2	439.8	44.2	990	3 US-09-974-300-1719	Sequence 1719, Ap
3	287.8	28.9	984	7 US-10-282-122A-9120	Sequence 9120, Ap
4	237	23.8	969	7 US-10-282-122A-9817	Sequence 9817, Ap
5	232.6	23.4	990	7 US-10-398-221-766	Sequence 766, App
6	232.6	23.4	990	7 US-10-398-221-2682	Sequence 2682, Ap
7	232.6	23.4	990	7 US-10-282-122A-24755	Sequence 24755, A
8	173.8	17.4	1616	6 US-10-429-802-17	Sequence 17, Appl1
9	173.8	17.4	1616	6 US-10-430-503-8	Sequence 8, Appl1
10	160.2	16.1	978	7 US-10-282-122A-34300	Sequence 34300, A
11	159	16.0	996	7 US-10-724-972A-1455	Sequence 1455, Ap
12	146	14.7	993	7 US-10-282-122A-1455	Sequence 7960, Ap
13	146	14.7	11466	2 US-08-781-986A-444	Sequence 444, App
14	146	14.7	11466	2 US-10-329-624-444	Sequence 444, App
15	142.8	14.3	1002	3 US-09-815-242-8383	Sequence 8383, Ap
16	142.4	14.3	981	3 US-09-815-242-4665	Sequence 4665, Ap
17	117.8	11.8	972	7 US-10-282-122A-35759	Sequence 35759, A
18	95.4	9.6	972	7 US-10-282-122A-20906	Sequence 20906, A
19	80.6	8.1	972	7 US-10-282-122A-21716	Sequence 21716, A
20	80.2	8.1	2256646	7 US-10-470-565-1	Sequence 1, Appl1
21	72.4	7.3	1050	7 US-10-282-122A-12199	Sequence 12199, A
22	63.6	6.4	978	7 US-10-398-221-911	Sequence 911, App
23	63.6	6.4	978	7 US-10-398-221-2826	Sequence 2826, Ap

24	61.8	6.2	579	7 US-10-282-122A-21539	Sequence 21539, A
25	55.2	5.5	1092	7 US-10-282-122A-40070	Sequence 40070, A
26	53.6	5.4	1092	7 US-10-282-122A-38691	Sequence 38691, A
27	52.2	5.2	9749	3 US-09-070-927A-154	Sequence 154, App
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29	47.8	4.8	400	7 US-10-329-624-3720	Sequence 3720, Ap
30	40.8	4.1	37973	6 US-10-311-455-2169	Sequence 2169, Ap
31	37.2	3.7	1068	3 US-09-815-242-6788	Sequence 6788, Ap
32	37	3.7	10528	6 US-10-311-455-307	Sequence 307, App
33	36.4	3.7	61662	6 US-10-418-837-1	Sequence 1, Appl1
34	36.4	3.7	61663	5 US-10-114-170-62	Sequence 62, Appl1
35	36	3.6	826	3 US-09-070-927A-799	Sequence 799, App
36	35.8	3.6	353	3 US-09-925-065A-392869	Sequence 392869, A
37	35.8	3.6	3673778	6 US-10-312-841-2	Sequence 2, Appl1
38	35.4	3.6	245	3 US-09-080-107-1689	Sequence 1689, Ap
39	35.4	3.6	419	4 US-09-925-065A-654182	Sequence 654182, A
40	35.4	3.6	419	4 US-09-925-065A-654183	Sequence 654183, A
41	35	3.5	600	9 US-10-972-079-44650	Sequence 44650, A
42	35	3.5	961	7 US-10-648-593-102	Sequence 102, App
43	35	3.5	1053	9 US-10-450-763-28412	Sequence 28412, A
44	35	3.5	11036	5 US-10-239-676-118	Sequence 118, App
45	35	3.5	11036	6 US-10-240-453-138	Sequence 138, App

ALIGNMENTS

RESULT 1
US-10-812-387-1
Sequence 1, Application US/10812387
Publication No. US20050142652A1
GENERAL INFORMATION:
APPLICANT: SIVARAMAN, HEPHIZIAH
APPLICANT: PUNDRE, ARCHANA VISHNU
APPLICANT: SURBESH, CHERAVAKKATTU GOPALAN
APPLICANT: DODSON, GEORGE GUY
APPLICANT: BRANNIGAN, JAMES ANTHONY
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF LARGE AMOUNT OF PENICILLIN V
FILE REFERENCE: 056859-0196
CURRENT APPLICATION NUMBER: US/10/812,387
CURRENT FILING DATE: 2004-03-30
PRIOR APPLICATION NUMBER: PCT/IB03/06198
PRIOR FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 1
LENGTH: 996
TYPE: DNA
ORGANISM: Bacillus subtilis
US-10-812-387-1
Query Match 100.0%; Pred. No. 1.6e-289; Length 996;
Best Local Similarity 100.0%; Mismatches 0; Gaps 0;
Matches 996; Conservative 0; Indels 0; Gaps 0;
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Db 1 CATATGTGCAAGTCTTACATTTGAACTGCTACCGTAAACATGATATTAGACAGAAC 60
QY 61 ATGATTTTGCATTGACCTGCGGACAGAGCTATCTATCCGCGCTTACAGCTGG 120
Db 61 ATGATTTTGCATTGACCTGCGGACAGAGCTATCTATCCGCGCTTACAGCTGG 120
QY 121 AATAGTGAAGCTGACGGAAGGCGCCATCGACACATGACGCTTATCCGTATGAGGAG 180
Db 121 AATAGTGAAGCTGACGGAAGGCGCCATCGACACATGACGCTTATCCGTATGAGGAG 180
QY 181 AAACCTGGAATATATTTATTTGCGGACGCGCATTAATGAAGCGTTATCTTGCGCG 240
Db 181 AAACCTGGAATATATTTATTTGCGGACGCGCATTAATGAAGCGTTATCTTGCGCG 240
QY 241 CTTTATTTTCCGGGCTATGCGAGTACGAAAAAAGATACGGGAAGATACCTTCACATT 300
Db 241 CTTTATTTTCCGGGCTATGCGAGTACGAAAAAAGATACGGGAAGATACCTTCACATT 300


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Db      301 GTCCCGCATGATTTGTGACATGGGTGCTGCAAGTCTGTCACTTTTGGAAAGCGTAAA 360
Qy      361 GAAAGAGTGCATCTTTAACAATGTGTAGAGAAAAAATAGATCTATGGATACGTTTAA 420
Db      361 GAAAGAGTGCATCTTTAACAATGTGTAGAGAAAAAATAGATCTATGGATACGTTTAA 420
Qy      421 CCGCTTCACTGATATTTGTACAGCCGAGCGGGCCGAAACTGACGATGAACCAAGACA 480
Db      421 CCGCTTCACTGATATTTGTACAGCCGAGCGGGCCGAAACTGACGATGAACCAAGACA 480
Qy      481 GACGGCTCAAAAGTGTATGATATATCACTGTGTATGATGAGACAGACCCGACCTTTTA 540
Db      481 GACGGCTCAAAAGTGTATGATATATCACTGTGTATGATGAGACAGACCCGACCTTTTA 540
Qy      541 TGGCATGTATCAATCTGCAGCATATATACAGGAATCAGACCGAAGCAATTAAGAGACAA 600
Db      541 TGGCATGTATCAATCTGCAGCATATATACAGGAATCAGACCGAAGCAATTAAGAGACAA 600
Qy      601 GAGATGGCGGATTAAGCCCTTCTGCTTTTGGCCAGGCTTAAAGACTGTGTGCTGCG 660
Db      601 GAGATGGCGGATTAAGCCCTTCTGCTTTTGGCCAGGCTTAAAGACTGTGTGCTGCG 660
Qy      661 GGGGATTAACACCGCCCTTCCGGTTTGTGACAGCTGTTTATTTGAAAGACATCTAAG 720
Db      661 GGGGATTAACACCGCCCTTCCGGTTTGTGACAGCTGTTTATTTGAAAGACATCTAAG 720
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Db      721 CCGGGCGCGCATGAAGAGAGATGTAAACAGCCGCTTTCAAAATTTTGGCAATATGACG 780
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Qy      901 AAGATTAATTTTATTCATGAGAGACCTTGAAGCTTTGAGACCTTAAAGTGTTCGCTAAA 960
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RESULT 2
US-09-974-300-1719
; Sequence 1719, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Beirka, Randy M.
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1719
; LENGTH: 990
; TYPE: DNA

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; ORGANISM: Bacillus licheniformis
US-09-974-300-1719
Query Match      44.2%; Score 439.8; DB 3; Length 990;
Best Local Similarity 65.3%; Pred. No. 1.5e-121;
Matches 645; Conservative 0; Mismatches 342; Indels 0; Gaps 0;

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Qy      64 GATTTGCAATTTACGCTGGGAGACAGAGTATCTCTATCCGCCCTTACAGCTGAGAC 123
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Qy      124 AGTGAAGTGAACGGAAGGAGCCATCAAGACAGATACCGCTTATCGGATAGGAGAA 183
Db      121 AGTGAAGGAGAGGAGAGAGAGATGCGGCGGATGATGCGGATAGGAGAG 180
Qy      184 CTTGAAATATATATTTATTTGCGAGCGCATTAATGAAACGGTTTATCTTGTGCGCGCTT 243
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Qy      304 CCGATGAGTTTGTGACATGAGGCTGTGCACTGTGATGCTTGTGAGAGAGTAAAGAA 363
Db      301 CCGACGAAATTCGAGATGAGGTCTGTGAAATGCGCGATTTGAGAGAGTGAAGAAA 360
Qy      364 AAGATTCGATCTTAAACATTTGAGAGAAATTAATCTATTTGATACGTTTACCG 423
Db      361 GCGGCTGTTCTTAAACATTTGAGAGAGAGGTGACGCTTGTGATGAGTACGTCGCG 420
Qy      424 CTTGACGTGATTTGTGACAGACCGGACCGGAAACCTGAGATAGAACCAAGACGAC 483
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Qy      484 GGCCTCAAGTCTATGATATCAACCTGTGTGATGAGAACAGCCCGACCTTTATATG 543
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Qy      544 CATGTAAACCAATCTGACCAATATACAGAAATCAGACCGAAGCAATTAGACGAAAG 603
Db      541 CATTTGACCAATTTGCGCACTTATACGCTCTTACGCGGACAGTGTTCGCGAAGAAA 600
Qy      604 ATGGGCGATTAAGCCCTTCTGCTTTTGGCCAGGCTTAAAGACTGTGTGCTGCGGG 663
Db      601 ATGGGAGGCTGACGCTGTGCGCTTTTGTGCAAGGTTCCGGGCTGTCCGATTTGCAAG 660
Qy      664 GATTAATACAGCGCTTCCCGGTTTGTGACAGCTGTTTATTTGAAGAAACATCTAGAGCG 723
Db      661 GATTTTACGCGCATCTCCGCTTTTGTGACAGGCTGATTTTGAAGAGACATGAAGCT 720
Qy      724 GCGGCGATGAAACGAAAGGTGTAAACAGCCGCTTTCAATTTTGGCAATATGAGATA 783
Db      721 GTGTCCGATGAAACGAAAGGCTCTCTCCGCGTTTCAATCTCTCCCAATATGATAT 780
Qy      784 CCAAGGCGCGCATGTATACGGAAGAACGAAATTCCTTAAAGCAATATATCTTCCG 843
Db      781 CCAAGGCGGTGTATGATGATCAAGGCGGAAGCAATTAACCAATATACGCGGAT 840
Qy      844 ATGTGCAAGAACTGAAACTACTATTTCCACCACTATGACATCGGCAATCCAAAA 903
Db      841 ATGTGACAGGAGACGTGACGATCTATTTTCACTATTAACAAACAGGCAATTCAAA 900
Qy      904 GTAAATTTATTTCAATGAGACCTTGAAGCTTTGAGACCTTAAGTGTTCGCTAAAGCA 963
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Qy      964 GAAAGAGATTCATGAGCTTAATTA 990

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Db 961 GAAGAGACGGTTCATTCTTCAATCA 987

RESULT 3

US-10-282-122A-9120

Sequence 9120, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9120

LENGTH: 984

TYPE: DNA

ORGANISM: Bacillus anthracis

US-10-282-122A-9120

Query Match 28.9%; Score 287.8; DB 7; Length 984;

Best Local Similarity 56.0%; Pred. No. 1.2e-75;

Matches 544; Conservative 0; Mismatches 427; Indels 0; Gaps 0;

4 ATGTGCAAGTCTTACATGGAACCTGACCGTAAACATGATTAAGCAAGACATG 63

1 ATGTGATCTAGTGTGACATTAAGCAAAAAAGGTGACATCTTTTGAAGACATG 60

64 GATTTGCAATTCAGCTGGGAGACAGAGTATCTTATCCGCGCCGTTACAGCTGAC 123

61 GACTTCACTTAGTATGATCAAGAGTAAATATCACTTCTCGACATTAACAGTGAAT 120

124 AGTGAAGCTGACGGAAGGCGCATCAACACAGTACCGCTTTATCGTATGGGAGAAA 183

121 AATATTAACGGGTAAATCATTAATACGAAACATGCTACGATCGGAATGGGTATTAATCAT 180

184 CTGGAATATATATTTTGGCAGCGGCAATTAATGAAGCGTTTATCTTGGCGGCGCT 243

181 CAAGAGAGATCTTATGCGGAGCGAGTAAATGAACAGATATGACATGCAACATC 240

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QY 424 CTTCATGATATTTGTGACACCGGACGGCGGAAACCTGACGATGAAACCAAGACAGAC 483

Db 421 CTACATTTGATTTTGAAGGATTAATGGGAGATTGCTATGATCTGATCCGACAAAGTGA 480

QY 484 GGCCTCAAGCTCTATGATTAATCAACCTGTGTATGACGACGACGCCCACTTTATATGG 543

Db 481 GAATTAATAATTTGATGATTAACCACTAGAGTATGACGATATGTCGAGATTTAATTTGG 540

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Db 541 CATTTACAAATTTTAAAGCAATATAGGCTTAAATCGACGATTCGGGCCCAACAGAG 600

QY 604 ATGGCGGATTAAGCCCTTTGCTTTGGCTTTGGCCAAAGGCTTAGAACTGTGGCTTGGCGGG 663

Db 601 TGAGTAATTTTACCATTAAGTGTGCTTTGGCCAAAGGCTCGGGCTCAATGGAGCTTCCAGGG 660

QY 664 GATTTATCAACCGGCTTCCGGTTTGTCAAGGCTGTTTATTTGAAAGCACTTAGAGCCG 723

Db 661 GATTTTCAACCCCGCATCGAGGTTTGTGCGGGAGCATATGGAACAAACATTCAGAGT 720

QY 724 GCGGCGGATGAACGAAGGTGTAACGCGGCTTTTCAATTTTGGCAATATGACGATA 783

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QY 844 ATGTGCAAGAACTGGAATCTATTTTCCACCATATGACATGCGCAATTCACAAA 903

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QY 964 GAAGAGATAT 974

Db 961 AATCAAAAAAT 971

RESULT 4

US-10-282-122A-9817

Sequence 9817, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9817
LENGTH: 969
TYPE: DNA
ORGANISM: Bacillus anthracis
US-10-282-122A-9817

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Query Match 23.8%; Score 237; DB 7; Length 969;
Best Local Similarity 55.5%; Pred. No. 2.5e-60;
Matches 538; Conservative 0; Mismatches 425; Indels 6; Gaps 4;

QY 4 ATGTGACAAAGCTTACATGGAAACTGCTGACCGTAAACATGATTTAGCAAGAAATG 63
DB 1 ATGTGTACTAGTTGACATTAAGACAAACCGCTGACATCTTTTGCAGAAACGATG 60
QY 64 GATTTTGATTTGACCTGGGACAGAGGTGATTCCTGCGCGCGCTTACAGCTGAGAC 123
DB 61 GACTTCACATTAAGATTAATCAAGAAAGTAAATCAATTCCTGACATTAACAGTGAAT 120
QY 124 AGTGAAGCTGACGGAAGGCCCATCAGACACAGTACGCGTAAATGCGTAATGGGAGAAA 183
DB 121 AATATTAAGGGTGAATCATTAATACGAACATGCTACGCTGGAAATGGTATTAATCAT 180
QY 184 CTGGAAATATATTAATTTGCGCAGCGCATTAATGAAGCGGTTTATCTTTGCGCGCTT 243
DB 181 CAGGAAGGATCATTAATGCGCGAGGAGTAATGAAGCGATATGACATGTGCACACATC 240
QY 244 TATTTTCCGGGCTAATGCGGAGTAACAAAAACGATACGGAAGATACCGCTTACATGTG 303
DB 241 TATTTTCCAGGATTCGCTACTATATGTCMAAGCATATAGAACACAAAGAAATTTGGCT 300
QY 304 CCGCATGATTTGTGACATGGGCTGTCACTCTGTCACTCTT--GGAAGACGTAAAG 361
DB 301 CCATTTGATTTTGTAACTTGGAGTCTGACACAAATTCATTTCTGTCAAGGCCAGTGAAGA 360
QY 362 AAAAGATTCGATCTTTAACGATTTGAGAAAAAATTAGATCTATTTGATAC-AGTTTAA 420
DB 361 AATCTGTAGATGACATTAACCTTTTGTGATATACATTAACCGCATTTAGACTTACGCCA 420
QY 421 CCGCTTCACTGATATTTGACAGCGGAGGCCGAAACCTGACGATTAACCAAGAGAGA 480
DB 421 CCACATACATTTGATTTTACCGGATTAATGGGAGATTTGATTTGATCTGACGACAGT 480
QY 481 GAGGCGCTCAAGCTCTATGATATCAACTGTGTCTATGACGAACAGCCCGCATTTTATA 540
DB 481 GAGGATTTAAATTTGATATTAACCACTAGAGATGATACGAATATGTCCGAGTTTAAAT 540
QY 541 TGGCATTTAACAATCTGACAGCAATTAACAGAAATGACCGAAGCAATTTAGAGACAAA 600
DB 541 TGGCATTTTCAAAAATTTAGACAAATATATATAGGCTTAAATGCGCATTTCGCGCCACAA 600

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QY 601 GAGATGGCGGATTAAGCCCTTCTGCTTTTGGCCAAAGCTTAGAACGTGTGCTGCGG 660
DB 601 GAGTGAAGTAAATTAATCATTAATGCTTTTGGCCAAAGCTGCGGCTAAATGGGACTTCCA 660
QY 661 GGGGATTTAATACCGCTTCCCGTTTGTGACAGCTGTTTATTTGAAAGAACATCTAGAG 720
DB 661 GGGGATTTACCCCGCATCAGAGTTGTGCGGCGACAGCAATATGCAACAAACATTCMA 720
QY 721 CCGCGCGCCGATGAAGAGAGTGTACAGCCGCTTTTCAAAATTTGGCAAAATATAGAG 780
DB 721 GGTATATATAGCAGAAAGAGGAGTACAGCCCTTTTCAATCTTATCAAAATTTGAG 780
QY 781 ATACCAAGGCGGAGTATTAACGGAAGAGACGAATTCATTAATACCAATATA-CTTC 839
DB 781 GTTCTTAAGTGAAGTAAATTAACGAACAAAGGTGACATTAATATACCAATATACCAAG 840
QY 840 CGTATGTGCAACGAACGGAACCTAATCTTTCACCACTATAGACAAATCGG--CAATC 897
DB 841 CGTATGTGATGGAATCCGGAACATATTTATCTTACTTACAAATGTAGACCAATTA 900
QY 898 CAATAAGTAATTTATTCATGAAAGACCTTGACTTTGAGAGCTTAAAGTGTTCGCT 957
DB 901 TAGCTTGTCAATTAATTTCTGAAATTTAGATACCAATGAATTAAGCTTATCCCTTC 960
QY 958 AAACGAGAA 966
DB 961 CCACCGGAA 969

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RESULT 5
US-10-398-221-766
Sequence 766, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 766
LENGTH: 990
TYPE: DNA
ORGANISM: Listeria monocytogenes-BGD
US-10-398-221-766

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```

Query Match 23.4%; Score 232.6; DB 7; Length 990;
Best Local Similarity 53.0%; Pred. No. 5.5e-59;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY 4 ATGTGACAAAGCTTACATGGAACCTGACCGTAAACATGATTTAGCAAGAAATG 63
DB 1 ATGTGACAAAGCTTGTATTAAGAAAGCTTAAGGAACAACTTTATTAACAAAGCATG 60
QY 64 GATTTTGATTTGACGCTGGGACAGAGGTGATTCATTCGCGCGCTTACAGCTGGAAC 123
DB 61 GATTTTGCTTTTATTTTGAAGGCGAACCAACATTAACCCMAAGAAATTAATGATGAGAA 120
QY 124 AGTGAAGCTGACGGAAGGCCCATACAGACAGTACGCGTTTATGCGTAATGGGAGAAA 183
DB 121 TCTTCTACAGACGCGCATTAATTAATATATATATGATTTGAGCGGAGAGAGAG 180
QY 184 CTGGAAATATATTAATTTGCGGACGATTAATGAAACCGGTTTATCTTTGCGCGCTT 243
DB 181 TTAGTAAATATCAATTTTGCAGACGAGATTTGAATGAAGAAATTAAGCTGTGCAATCTCA 240

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OY 244 TATTTTCCGGGCTATGCGGAGTACGAAAAACATACGGGAAGTACCGTTCATGTC 303
 Db 241 TATCTTCCAGGAGAACGACGTTTATGCGCCACACACAGTGAAGGAAAAATCATTTTACGT 300
 OY 304 CCGCATGAGTTTGTGACATGGGTGCTGTCAGTCTTGTGGAAGCGTAAAGAA 363
 Db 301 CCACAGAATTTTGTGCTTTGGCTGTGAGAACTTGGCCACAGATTAAAGATGTGAAGCA 366
 OY 364 AAGATTGCATCTTTACGATTGTGAGAAATAATTGATCTATTTGATACAGTTTACCG 423
 Db 361 AAGTTATCGGTTATTAACCTTGGGAGTCAACCAAGTACCGTTACTTGAATCACAAACCA 420
 OY 424 CTTCACGTGATATTGTCAAGCCGAGCGGCCGAACCTGACGATAGAACCAAGACGAC 483
 Db 421 TTACACTGGATTTTCAACAGCAAGAGTGGCGTGTGTGATGATTGAACCAAGAAACA 480
 OY 484 GGGCTTCAAAGTCTATGATTAATCAACTGTGTCTATGACCAACAGCCCGCATTTATATGG 543
 Db 481 TCGCTTCGTATTAATAAATAAAACCTGTAGAGTTTATGACAAATACGCCACGATCGAATGG 540
 OY 544 CATGTAAACCAATCTGCAGCAATATACAGCAATCAGACCGAAGCAATTAGAGACAAAGAG 603
 Db 541 CATATCGAAGATTTTACGAACATACAGGTTTACAGCAACACATTTAAGGCCGGGTGAAG 600
 OY 604 ATGGGCGATTAGCCCTTTCTGCTTTTGGCCAAAGCTTAGAACTGTGTGTCGCCGGGG 663
 Db 601 TTCGAGAGATATATGCGTAAACCATTTTGGCAAGGTACAGGAACAAGCAATTAACAAGGT 660
 OY 664 GATTATACACGCGCTTCCCGGTTTGTCAAGCGTTTATTTGAAAGAACCTTAGAGCCG 723
 Db 661 GGTATATCTCCGCCAGAACGTTTTTGTCCGTGCCGCAATCTTGAAGAAAATATTAATAAA 720
 OY 724 GCGGCGGATGAACGAAGAGTGTACAGCCGCTTTTCAATTGTGGCAATATAGAGAT 783
 Db 721 GCGAATAAACGAAGAGAGACCTATCAAAATGTGTGGTATGTCTTGAACAGTGTCCGCAAT 780
 OY 784 CCAAGAGGGGCGAGTGTAAACGAAGAAAGACGAATCATTAATCGGAATTACTTCGTG 843
 Db 781 CCGAATGAGCCGTATTTAAAGAAAGTGTGACCTTGATTTTCAACAAATATGTGGCATCT 840
 OY 844 ATGTGCAACGAACCTGGAACCTACTATTTTCCACCACTATGACATCGGCAATCCAAAA 903
 Db 841 ATGTGTGCGAAGCAACCAACGTACTATTTTCACTCATACGAATAACCAACCAATCAATAAG 900
 OY 904 GTAAATTTATTTACAGAAACCTTGACTGTGTTGA 938
 Db 901 GTTACTTGTGCAAGAGATTTATAGAAATATATGA 935

```

RESULT 6
US-10-398-221-2682
Sequence 2682, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 US
CURRENT APPLICATION NUMBER: US/10/398, 221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 2682
LENGTH: 990
TYPE: DNA
ORGANISM: Listeria monocytogenes EGDc
US-10-398-221-2682

```

Query Match 23.4%; Score 232.6; DB 7; Length 990;

Best Local Similarity 53.0%; Pred. No. 5.5e-59;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

OY	4	ATGGCAACAGTCTTACATTTGGAAACTGTGACCCGTAACAGTATTTGACAAACATTTG	63
OY	4	ATGGCAACAGTCTTACATTTGGAAACTGTGACCCGTAACAGTATTTGACAAACATTTG	63
Db	1	ATGGCAACAGTCTTACATTTGGAAACTGTGACCCGTAACAGTATTTGACAAACATTTG	60
OY	64	GATTTTCATTTGACCTGGGGGACAGAGTATCTCTATCCGGCCGTTACAGCTGGAAC	122
Db	61	GATTTTCATTTGATTTGGAGGGCAACCCAAACAATTAGCCCAAGAAATTAATGATGAAA	12
OY	124	AGTGAAGCTACGGAAGGGCCCATGAGACACAGTACGGCTTTATCGGTATGGGGAGAAA	18
Db	121	TCTTCTACACACCGTCCCAATTATTAATAGATATGCAATTTGTGGAGCGGGAAGAG	18
OY	184	CTTGGAAAATATATTAATTTGCGCAGCGCATTAATGAAAAGGGTTATCTTTGCGCGCTT	24
Db	181	TTAGATTAATAACATTTTCGACACGGATTTGAATGAAAGATTAAGCTGTGCATCTTA	24
OY	244	TATTTTCCGGGCTATGCGGAGTACGAAAAACGATACGGGAAGATACCGTTCACATGTGC	30
Db	241	TATCTTCAGAGAAACAGTTATATGCGCAGCACACAGTGAAGAAAATACATTAAGCT	30
OY	304	CCGATGATTTTGTGACATGGGTGCTGTACGTCTCATGTCTTTGGAAGAGTAAAGAA	36
Db	301	CCACAGAAATTTTGTGCTTGGCTGTATGGAACCTTCGCAACGATTTAAAGATGTGAAACA	36
OY	364	AAAGTTGCATCTTTACGATGTGAGAGAAAAAATTAGATCTATTGGATACAGTTTACCG	42
Db	361	AAAGTTATCGGTTATTAACCTTGGTGAATCAACAGTACCGTTATTTGGAATCACACACA	42
OY	424	CTTCACTGATATTTGTACAGACCGGACGGGCCGMAACTGACGATGAAACCAAGACAGAC	48
Db	421	TTTCACTGATATTTGTACAGACAGAGTGGGGGTGTGATGATTTGAACCAACGAAACA	48
OY	484	GGCTCAAAAGTCTATGATTAATCAACCTGTGTGATGACGAACAGCCCGCATTAATATG	54
Db	481	TGCGTTCTGATTAATAAAMAAACCCTGATGAGATTAAGCAAAATACGCCACGATCGAAATGG	54
OY	544	CATGTAACCAATGTGACGATATTAACGGAATCAGACCGGAAGCAATTAGAGACGAAGAG	60
Db	541	CATATGAGATTTTACGAACTACACAGTTTACAGCAACACAAATTAGCCCGGTGAAG	60
OY	604	ATGGGCGAATTAGCCCTTTCTGCTTTTGGCCAGGCTTAGGAACCTGTGTCTGCGGGG	66
Db	601	TTGGAGAGATATATGCTTAACCAATTTTCGAGGTAACGGAACAAGAAATTAACAGGT	66
OY	664	GATTAATACACCGCTTCCCGGTTTGTCAAGCTGTTTATTTGAAAAGAACATCTAGACCG	72
Db	661	GGTTAATCTCCGCAAGAACGTTTGTTCGTGGCGCATCTTGAAGAAAATATTAATAAA	72
OY	724	GGCGCCGATGAAACGAAGGTGTAACGCGCTTTCAAAATTTGGCAAAATATGACATA	78
Db	721	GCGAAAAACGAGAGAGACCTATCAAAATGTGTGTATGCTTGAACAGTGTCCGATTT	78
OY	784	CCAAAGGGCGCAGTGATTAACGGAAGAACGAATTCATTAACGCAATATATCTTCGTG	84
Db	781	CCGAATGGAGCGGTATTAAGAAAGTGTGACCTGATTTCAACACAATATGTGGCATCT	84
OY	844	ATGTGCAAGAACTGGAAAATTAATTTTCCACCACTATGACAAATCGGCAATCCAAAA	90
Db	841	ATGTGTTCCGAAAGCAAAACGTAATTTTCACTCATTCGAAAAACAACCAATCAATAGT	90
OY	904	GTAATTTATTTCAATGAGACCTTACATGCTTTTGA	938
Db	901	GTTACTTTGTCAAGAGATTAATAAATAATGAA	935

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RESULT 7
US-10-282-122A-24755
; Sequence 24755, Application US/10282122A
; Publication No. US80040029129A1
; GENERAL INFORMATION:

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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24755
LENGTH: 990
TYPE: DNA
ORGANISM: Listeria monocytogenes
US-10-282-122A-24755

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Query Match 23.4%; Score 232.6; DB 7; Length 990;
Best Local Similarity 53.0%; Pred. No. 5.5e-59;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY 4 ATGTGACAAGCTTACATTGGAACCTGCTGACCTTAACATGTATAGCAAGAACATG 63
DB 1 ATGTGACAAGCTTACATTGGAACCTGCTGACCTTAACATGTATAGCAAGAACATG 60
QY 64 GATTTCGATTCAGCTGGGACAGAGGTGATTCCTATCCGCGCTTACAGCTGGAAC 123
DB 61 GATTTCGATTCAGCTGGGACAGAGGTGATTCCTATCCGCGCTTACAGCTGGAAC 120
QY 124 AGTGAAGCTGACGGAAGGGCCCATCAGACACATAGCCGTTATCGTATGGGAGAAA 183
DB 121 TCTTTCACAGACGCTCCCATTTATTTATAGATATAGCATTTTGGAGCGGGAAGAG 180
QY 184 CTTGGAATATATATTTTGGCCGACGATTAATGAAGCGTTATCTGTGCGGCGCTT 243
DB 181 TTGATTAATATCTTTTGGACGACGATTAATGAAGCGTTATCTGTGCGGCGCTT 240
QY 244 TATTTTCGGGCTATGCGAGTACGAAAAACATACGGAAGATACCGTTCACTGTC 303
DB 241 TATCTTCAGAGAGAGAGATTATGCGCCAGACCAAGTGAAGAAAAATCAATTTAGCT 300
QY 304 CCGCATGAGTTTGTGACATGGGTGCTGTCACTGTCTGACGCTTTGGAAGAGCTAAAGAA 363
DB 301 CCAAGAAATTTTGTGCTTGTGCTGTAGGAATTTGGCCAAAGATTAAGATGTGAGCA 360

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QY 364 AAGATTGCATCTTAAACGATTGTAGAGAAAAATTAGATCTATTGATACGTTTACCG 423
DB 361 AAGTTATCGTTTAAATCTGTGTGATCAACCACTACCGTTACTGTGAATCAACACCA 420
QY 424 CTTGACGTGATATGTGACACCGGACCGGAAACCTGACGATAGAACCAAGACAGAC 483
DB 421 TTACACTGGAATTTTCAACAGACAGAGGTGGCGTTGTGTGATGATTTGAACCAAGAAACA 480
QY 484 GGCCCTCAAAAGTCTATGATATCAACCTGTGTCTATGACGAACAGCCCGCACTTATATG 543
DB 481 TCGCTTGATTAATAAAGAAACCTGTAGAGTTATGACAAATACGCCACGATCGAATG 540
QY 544 CATGTAACCAATCTGACGCAATATACAGGAATCAGACCGAAGCAATTAAGAGCAAGAG 603
DB 541 CATATCGAATTTTACGCAATACAGGTTTACAGCAACACATTAAGCCCGGTGAAG 600
QY 604 ATGGCGGATTAAGCCCTTTCCTTTGGCCAGGCTTAGAAGCTGTGCTCGCGGG 663
DB 601 TTGGAAGTATATGCGTAAACATTTTCGACAGGTACAGAACAGCAATTAACAGGT 660
QY 664 GATTATACACCCCTTCCCGTTTGTCAAGCTGTTTATTTGAAAGAAATCTAGAGCGG 723
DB 661 GGTATATCTCGCCAGAACGTTTGTCCGTGCGCATCTGAAAGAAATATATATAAA 720
QY 724 GCGGCCGATGAAGAAAGGTGTACAGCCGCTTTCAATTTTGGCAAAATATAGCAT 783
DB 721 GCGAAAGAGAAAGAAAGGTATACAAATGTGTGTATGCTTGAACAGTGTCCGCAAT 780
QY 784 CCAAGGGCGAGATATACGGAAGAAAGCAAAATTCATTAACCAATATATCTTCCGTG 843
DB 781 CGAATGAGCGGTATTAAGAAAGGTGTACCTGATTTTCAACCAATATGTGCACT 840
QY 844 ATGTGACAAGAACTGGAACCTACTATTTCACCACTATGACATCGGCAATCCAAAAA 903
DB 841 ATGTGTTGGAAGAAAGCAATCTATTCACCTATGCAAAACCAACCAATCAATAGT 900
QY 904 GTAATTTATTTTCAAGAAAGCTTGCATGCTTTTGA 938
DB 901 GTTACTTGTGAGAGAGTTATAGAAATATAGAA 935

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RESULT 8
US-10-429-802-17
; Sequence 17, Application US/10429802
; Publication No. US2003022825A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YITU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSC:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/377,672
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 1616
; TYPE: DNA
; ORGANISM: Bacillus sphaericus
; US-10-429-802-17

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Query Match 17.4%; Score 173.8; DB 6; Length 1616;
Best Local Similarity 49.8%; Pred. No. 4.1e-41;
Matches 495; Conservative 0; Mismatches 492; Indels 6; Gaps 2;

QY 7 TGCAGAGCTTATCACTTGAAGCTGACCGTAAACATGTATTTAGCAAGAACATGAT 66
DB 335 TGCAGAGCTTATCACTTGTACCAAGATGATTAAGTTATTTGCTGCGCAATGAT 394
QY 67 TTTGATTTCACTGGGAGCAGAGGTGATTCCTCTATCCGCGCGTTACAGCTGAACAGT 126

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Db 395 TTTACATGACAGATAGTAAGTATATATGTCCTCCAGTAATTAACGCAATTCGATG 454
 Qy 127 GAAGCTGACGAA--GGGCCATCAGACACAGAACCGGTTATCGGTATGGAGAA--181
 Db 455 TTAGAAAAAGAAATGATGATTAACATTCATATGCTTTGTTGGAATGGAGAGCT 514
 Qy 182 -AACTGGAAATATATATTTGCGGACGCAATTAAGAACGGTTATCTTGGCGCG 240
 Db 515 GACATTCATCAGACAGTCTCTATGATGGGGTAAACGAAAGGATTAATGGCGCAATG 574
 Qy 241 CTTATATTTCCGGGCTATGCGAGTACGAAACGATACGGAAGATACGTTCACTT 300
 Db 575 CTTTACTATGTAATTTCTCAAGTTTGAATGTTGTAACGTCGATGATGATTTAT 694
 Qy 301 GTCCCGATGATTTGTCAGATGGGTGCTGTCAGTCTGTCAGTCTTGGAGACGTAAA 360
 Db 635 AATCCGATGATGATTAATTTCTCAAGTTTGAATGTTGTAACGTCGATGATGATTTAT 694
 Qy 361 GAAAAATTCGATCTTTAAGATTTGAGAAAAATTAATGATCTATTTGATACGTTT 420
 Db 695 GAAAAATTAATCTTTATACATTTATGATGAGCCATATATATATCTGGCTTTGCAACC 754
 Qy 421 CCGCTTCACTGATATTTGTCAGACCGGACCGGACGAACTGACGATAGAACGAAGCA 480
 Db 755 CCACTTCACTATACATTTAAGATGCTTCTGTAATGATGATTTGTAACCGGATPAA 814
 Qy 481 GACGCTCAAAAGTCTATGATATCAACCTGCTGTCAGACGACGACCGGATTTATA 540
 Db 815 ACAGGCAATTCATTCATTCGAAAAACGATGGCGTCATGAGATAGCCGCTAGTAA 874
 Qy 541 TGGATATTAACCATTCGACGACATATACGAAATCAGACGGAAGCAATTTAGACGAA 600
 Db 875 TGGATATGACAAATTTAAGCTTACATTTGTCACACCAATTCGCCCAAGATATA 934
 Qy 601 GAGATGGGCGATTAAGCCCTTTCTGCTTTGGCCAGGCTTAGGAATGTTGGTCCG 660
 Db 935 ATGATGGAGACTTGGATTTGACACCGTTTGGGAGGAGGAGGCGGCTTAGATTAACA 994
 Qy 661 GGGATTAATACACCGCTTCCCGTTTGTCAAGCTGTTATTTGAAAGACATCTAGAG 720
 Db 995 GGTGATTTTACGCGTACAGACGTTTCTTGGGATGATCTGAAAAAATATATACGA 1054
 Qy 721 CCGGCGCGCATGAAGAAAGGTGTACAGCCGCTTTCAATTTGGCAATATAGACG 780
 Db 1055 AAAGCCAAATATGAACAGAAAGGCTTAACAACTGTTCCATATCTTCTGTAAAT 1114
 Qy 781 ATACCAAAAGGCGAGTATAGGAGAAAGAGAAATTCATTTATAGCAATATATCTCC 840
 Db 1115 ATCCCAAAAGGTGTTTGTGACAAATGAGGGGAAACGATATATACATCTATATCTCA 1174
 Qy 841 GTGATGTCAACGAACCTGAAACTATTTCCACACATATGCAATTCGCAATCCAA 900
 Db 1175 GCTATGTGACAAAGTAAATACTATTTAACTATGATGACATATGCAATTTCA 1234
 Qy 901 AAAGTAAATTTATTTATGAAACCTTGACCTTTGAGCCTTAAGCTTTTCCGCTAAA 960
 Db 1235 GCGGTTTCTTAAGGCTGAAATTTAAATAGTCMAATTTAATTAATTAAGTGGAT 1294
 Qy 961 GCAGAGAGATTTATGAGCTTAATTAAGA 993
 Db 1295 CTTAAACAGATTTAAGCAATTAATCAAGTA 1327

RESULT 9

US-10-430-503-8
 ; Sequence 8, Application US/10430503
 ; Publication No. US2004005684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUNG, MIEN-CHIE
 ; APPLICANT: LAN, KENG-LI
 ; APPLICANT: OU-YANG, FU
 ; APPLICANT: LIU, JAM-CHING
 ; APPLICANT: LAN, KENG-HSIN

; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
 ; REAGENTS
 ; FILE REFERENCE: US/10430503
 ; CURRENT APPLICATION NUMBER: US/10430503
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 60/383,063
 ; PRIORITY FILING DATE: 2002-05-06
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 1616
 ; TYPE: DNA
 ; ORGANISM: Bacillus sphaericus
 ; US-10-430-503-8
 Query Match 17.4%; Score 173.8; DB 6; Length 1616;
 Best Local Similarity 49.8%; Pred. No. 4,1e-41;
 Matches 495; Conservative 0; Mismatches 492; Indels 6; Gaps 2;
 Qy 7 TGCACAACTCTTACATTTGGAACCTGACCGTAAACATGATTAAGCAACATGAT 66
 Db 335 TGCAGTAGCTTATCAATTCGTACACAGATGATTAAGTTATTCGCTGCAATGAT 394
 Qy 67 TTTGCATTTAGCTGGGACAGAGTGTCTCTATCCGGCCGTTACAGCTGAAAGT 126
 Db 395 TTTACATGGAACCAATGATTAAGTATTTGTCACAGTAAATTAAGGCAATTCGAT 454
 Qy 127 GAAGCTGACGAA--GGGCCATCAGACACAGTAACGCTTTATCGGTATGGAGAA--181
 Db 455 TTAGAAAAAGAAATGATGATTAACATTCATATGCTTTGTTGGAATGGAGAGCT 514
 Qy 182 -AACTGGAAATATATATTTGCGGACGCAATTAAGAACGGTTATCTTGGCGCG 240
 Db 515 GACATTCATCAGACAGTCTCTATGATGGGGTAAACGAAAGGATTAATGGCGCAATG 574
 Qy 241 CTTATATTTCCGGGCTATGCGAGTACGAAACGATGATGATTTGTAACGCTTCACTT 300
 Db 575 CTTTACTATGTAATTTCTCAAGTTTGAATGTTGTAACGTCGATGATGATTTAT 694
 Qy 301 GTCCCGATGATTTGTCAGATGGGTGCTGTCAGTCTGTCAGTCTTGGAGACGTAAA 360
 Db 635 AATCCGATGATGATTAATTTCTCAAGTTTGAATGTTGTAACGTCGATGATTTAT 694
 Qy 361 GAAAAATTCGATCTTTAAGATTTGAGAAAAATTAATGATCTATTTGATACGTTT 420
 Db 695 GAAAAATTAATCTTTATACATTTAAGATGCTTCTGTAATGATGATTTGTAACCGGATPAA 814
 Qy 421 CCGCTTCACTGATATTTGTCAGACCGGACCGGACGAACTGACGATAGAACGAAGCA 480
 Db 755 CCACTTCACTATACATTTAAGATGCTTCTGTAATGATGATTTGTAACCGGATPAA 814
 Qy 481 GACGCTCAAAAGTCTATGATATCAACCTGCTGTCAGTCTGTCAGTCTTGGAGACGTAAA 540
 Db 815 ACAGGCAATTCATTCATTCGAAAAACGATGGCGTCATGAGATAGCCGCTAGTAA 874
 Qy 541 TGGATATTAACCATTCGACGACATATACGAAATCAGACGGAAGCAATTTAGACGAA 600
 Db 875 TGGATATGACAAATTTAAGCTTACATTTGTCACACCAATTCGCCCAAGATATA 934
 Qy 601 GAGATGGGCGATTAAGCCCTTTCTGCTTTGGCAAGGCTTAGGAATGTTGGTCCG 660
 Db 935 ATGATGGAGACTTGGATTTGACACCGTTTGGGAGGAGGCGGCTTAGATTAACA 994
 Qy 661 GGGATTAATACACCGCTTCCCGTTTGTCAAGCTGTTATTTGAAAGACATCTAGAG 720
 Db 995 GGTGATTTTACGCGTACAGACGTTTCTTGGGATGATCTGCAATTAATTAATCTGAA 1054
 Qy 721 CCGGCGCGCATGAAGAAAGGTGTACAGCCGCTTTCAATTTGGCAATATAGACG 780
 Db 1055 AAAGCCAAATATGAACAGAAAGGCTTAACAACTGTTCCATATCTTCTGTAAAT 1114
 Qy 781 ATACCAAAAGGCGAGTATAGGAGAAAGAGAAATTCATTTATAGCAATATATCTCC 840

Db 1115 ATCCAAAGGTGTTGTTTGAACAATGAGGGAAGGATTAACCATCTATACCTCA 1174
Qy 841 GTATGTCGAACGAACCTGGAACCTATGATTCACCACTATGCAACCGGACCAATCA 900
Db 1175 GCTATGTCGAACAAGTAACCTATTAAGCTATGACAAATGTCGAATTTCA 1234
Qy 901 AAGTAATTTATTTATTCATGAAGACCTTGACTGTTGGAGCTTAAGTCTTCCGCTAA 960
Db 1235 GCCCTTCTTAAAGCGCTGAATAATTAAATGTCAGATTTAATTAATTTAGTGGAT 1294
Qy 961 GCAGAGAGATTTATTCATGAGCTTATTAAGCA 993
Db 1295 CGTAACAGATATTAAAGCAATTAATCAAGTA 1327

RESULT 10
US-10-282-122A-34300
Sequence 34300, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zvekund, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 34300
LENGTH: 978
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34300

Query Match 16.1%; Score 160.2; DB 7; Length 978;
Best Local Similarity 49.9%; Pred. No. 4e-37;
Matches 458; Conservative 0; Mismatches 453; Indels 6; Gaps 2;

Qy 4 ATGTGCAACGCTTATTCATGGAACCTGCTGACCGCTTAACGATATTAACCAAGCAAG 63
Db 1 ATGTGTACGGCTATTTCTTATATACAAACACGTTATCATTTAGCTAGAACGATG 60

Qy 64 GATTTCATTTTCAGCTGGGAGACAGGTGATTTCTATTCGGCGCTTACAGCTGAAC 123
Db 61 GACTTTCATTTGATTTATTAATGATATCCCAACATTTGTCAGCTCATTTATCACTACAA 120
Qy 124 AGTGAAGCTGACGGAAGGCGCCATCAGACACATGACCGTTATTCGGTATGGGAGAAA 183
Db 121 TTTGATCTGATTTCA--GACATGCGCTTGAATATGTTTGTGGAACAAATTTAAA 177
Qy 184 CTTGGAATATATATTTATTTGCGGACCGCATTAATGAAGCGGTTATCTGTGCGCGCTT 243
Db 178 GTAGACGTTATATGATTTGTTGATGATATTAACGAAAAGGTTAGCTATTTGACACAT 237
Qy 244 TATTTTCGGGCTATGCGGAGTACGAAAACGATACGGAAGATACCTTCACATGTC 303
Db 238 TACTTCACTGGTGAAGGCTCATACATACCATTAACGTTATGTTTAACTTGA 297
Qy 304 CCGCATGATTTTGAATAGGTGCTCTCAGCTGTCAGCTTTGGAAGCGTAAAGAA 363
Db 298 CTTGAGAGATTTATTTGTTGGGTTTATGTTTAAATGAATTAAGCAATTTAAACAA 357
Qy 364 AAGATTCATCTTTAAGATTTGTAGAGAAAATTAATCATTTGATTAACGTTTAA 423
Db 358 AAGTTAAGAAAGATCATTTATTAATGAATGAABAAAATCACTTGAATATGTTCCGCT 417
Qy 424 CTTGATGATATTTGTGACACCGGACGGCCGAAACTGACGATGAACCAAGCAGAC 483
Db 418 TTACATTTCAATGCTCATGATGAACAGACATACCGTACCATGACCAACCTCAATGCGC 477
Qy 484 GCGCTCAAGCTATGATTAATCAACCTGCTGTCATGACGAAAGCCCGGCTTATATG 543
Db 478 TTATTAATGATTAAGATTAATTAATGTTCAATCACTTAACAAATGCGCTTAATTAATG 537
Qy 544 CATGTAAACATCTGCAGCAATATACAGAAATCAGACCGAAGCAATTAAGAGCAAGAG 603
Db 538 CATTTATCTAATCTTAAGAAATTAATGCTTATTTAACAACAGAAATCAACCAATTA 597
Qy 604 ATGGGCGAATTAAGCCCTTCTGCTTTTGGCCAGGCTTGAACCTGTTGCTGCGGG 663
Db 598 ATAGTAAAGTGTAGTAAGATCAATGGGTTGTACAGAGAAACAAATGCGCTTAC 657
Qy 664 GATTATCAACCGCTTCCGCTTGTGACAGCTGTTATTTGAAGAAACATCTAGAGCG 723
Db 658 GGTATATCTTAACAGAAAGTTTATACGGGCTCATTTTAAACACCACTACAGCTGT 717
Qy 724 GCGCCCATGAAGAAAGGTGTAAACAGCCCTTTCAATTTGGCAATATAGCAATTA 783
Db 718 TCCCATATGAAGATGAATTAATTAATGATTTTAAAGTTCTAGATCAGTCAATC 777
Qy 784 CCAAGGCGCAGTATACGGAAGAAAGCAAAATTTCTATTAAGCAATATATCTTCG 843
Db 778 CCAAGGCGCAGTATACGGAAGAAAGCAAAATTTCTATTAAGCAATATATCTTCG 834
Qy 844 ATGTGCAACGAACCTGGAATCTATTTTCCACACTATGACCAATCGGCAATCAACAAA 903
Db 835 ATGGAAGTAAAGAAAGAGCTATTAATTAAGCAATCTTATTAATCAATTTTCAA 894
Qy 904 GTAATTTATTTCAATGA 920
Db 895 ATAAATTAATCAAGAA 911

RESULT 11
US-10-724-972A-1455
Sequence 1455, Application US/10724972A
Publication No. US20040147734A1
GENERAL INFORMATION:
APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCI
FILE REFERENCE: PAT03-16
CURRENT FILING DATE: 2003-12-01

QY 124 AGTGAAGCTGACGGAAGGCCCATCAGACACAGTACGCGTTTATCGGTATGGGAGAAA 183
 DB 121 TCTCGCACT--GGCAGACAGGCCCAACGCAATATGCTTTATGTGTACAGAAACGAT 177
 QY 184 CTGGAAATATATATATTTGCGACGCGATTATGAAAGCGGTTTATCTTGCGCGCCTT 243
 DB 178 ATGGAAGCTTTATTTATGATGATGGTGTATTAATGAACATGGCGGTGATTTTGACACAA 237
 QY 244 TATTTTCGGGGCTATGCGAGTACGAAAAAAGATACGGAGATACCGTTTACATTGTC 303
 DB 238 TATTTCCGAGGTATATGATCATATGCTCAACACAAAGCGGACGGGATGAATATACG 297
 QY 304 CCGCATATGTTTGACATGGGTCTGTCACTGTGTGATCTTTGGAAGCGTAAAGAA 363
 DB 298 CAATATGAAATGTGACATGATTTGGATATACAAACAGCATTTGAATATACAA 357
 QY 364 AAGATTCGATCTTTAAGCATGTGTAGAGAAAAAATTAATCTATTTGATACAGTTTACCG 423
 DB 358 CAGCATCCCAATATACATGTTGTAGCGGTATTTAATATGATCGGTGAAGTTCCGCA 417
 QY 424 CTTCATGATATTTGTACAGCCGACCGGCGGAAACCTGACGATGAAACCAAGCAGAC 483
 DB 418 TTGCATTTATCATGTTCCGATGACATGACATTCAGTCGAAAGTTTCAATTTAAAGAGGG 477
 QY 484 GGCTCAAGTCATGATATCAACCTGGGTGTCAATGACGAAACAGCCCGCATTTATATG 543
 DB 478 GAAATGTTATTAATAAGATTAACCTTATGTTGTCTTAACTATTCAGATCTTGATTTGG 537
 QY 544 CATGTAACCATCTGACGCAATATATACAGAAATCAGACCGAAGCAATTAAGAGCAAAAG 603
 DB 538 CATATATGATTTAATGACATATATATCAATTTCTCTTATCCAGCAAGCAAAAGTTA 597
 QY 604 ATGGCGGATTAAGCCCTTTCTGCTTTTGGCCAGGCTTAGGAACTGTGTGCTCCGGGG 663
 DB 598 TTGAAGGTGTAAAGATTAACCTTTAGCAATGAAAGCAATGATTTGGAATTCGCAAGT 657
 QY 664 GATATATCAACGCTCTCCGCGGTTGTGAGCTGTTTATTTGAAGAAACATCTAGAGCG 723
 DB 658 GGAATTTACTTAACCTGACGCGCTTGTGTGAATTCGATTTATGAAGCAAACTTGCTCA 717
 QY 724 GCGCGCGATGAAGCAAGGTGTAAACGCGCTTTTCAATTTTGGCAATATATGACATA 783
 DB 718 AACATGATTAAGAAATGATTTATGAATGATTTTATTAATGATGCGGTAAATATA 777
 QY 784 CCAAGGCGCAGTGTATTAACGAGAAAGCAAAATTCATTATGCAATATATCTTCGCTG 843
 DB 778 CCGATTTGAATTTGATGCTCCGATGATGCTGCAATCACTATACATGTATACAGCCGTA 837
 QY 844 ATGTGCAACGAAACCTGGAACCTAATTTCCACGCTATGACCAATCGGCAATCCAAAA 903
 DB 838 ATAAATTTAATCTACAGAAACCTTATATATTAATTTATGCGACGAAATGATATAGCA 897
 QY 904 GTAATTTATTTTATGAGAACCTTGACTGTTTGAAGCTTAAAGTGTTCGCTTAAAGCA 963
 DB 898 TTAAGCTCAGACATGATTTATTAATGAAGAAATATGACATTTTAAAGCTGAGAG 957
 QY 964 GAAGAGATTTATCATGAGCTTAATTA 989
 DB 958 CATATCACTATTAGAAAGTTGAATGA 983

RESULT 13
 US-08-781-986A-444/c
 ; Sequence 444, Application US/08781986A
 ; Publication No. US20030054436A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5235
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville

STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248PP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 444:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11466 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-444

Query Match 14.7%; Score 146; DB 2; Length 11466;
 Best Local Similarity 47.5%; Pred. No. 2,9e-32;
 Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

QY 4 ATGTGCAAGCTTTACATTTGAAACTGCTGACCGGTAAATGATATAGAAAGCAATG 63
 DB 368 ATGTGCAAGCTTTACATTTGAAACTGCTGACCGGTAAATGATATAGAAAGCAATG 3629
 QY 64 GATTTTCATTTTACGCTGGGGAACAGAGGTATCTATCCGCGCTTACGCTGAAAC 123
 DB 3628 GATTTATATTTATTCATTTATGATGTTGCGCCAGCTGACGCTGAATTTATCGTTGAAA 3569
 QY 124 AGTGAAGCTGACGGAAGGCCCATCAGACACAGTACGCGTTTATGCGGTATGCGAGAAA 183
 DB 3668 TCTTCGCACT--GGCAGACAGGCCCAACGCAATATGCTTTATGCGACAGAAACGAT 3512
 QY 184 CTGGAAATATATATATTTGCGACGCGATTATGAAAGCGGTTTATCTTGCGCGCCTT 243
 DB 3511 ATGGAAGCTTTATTTATGATGATGTTATATGAACATGCGCTTGCCATTTCAACAAA 3452
 QY 244 TATTTTCGGGCTATGCGAGTACGAAAAAAGATACGGAAATACCGTTTACATTGTC 303
 DB 3451 TATTTCCGAGGTATATGATTTATGATCAATGAAACAAAGCGGAGGATGAATATTAAG 3392
 QY 304 CCGCATGATTTGTGACATGGGTCTGTCACTGTGTGATCTTTGGAAGAGCTTAAAGAA 363
 DB 3391 CAATATGAAATTTGACATGATTTGGGATATACAAACAGCATTTGAAGATATGACAA 3332
 QY 364 AAGATTCGATCTTTAAGCATTTGTAGAGAAAAAATTAATCTATTTGATACAGTTTACCG 423
 DB 3331 CAGCATCCCAATATACATGTTGTAGCTGTATATTTAATGACATGCGTAAGTTCCGCA 3272
 QY 424 CTTCATGATATTTGTACAGCCGACCGGCGGAAACCTGACGATGAAACCAAGACAGAC 483
 DB 3271 TTGCATTTATCATGTTTCCGATGACATGCAATACAGTGAAGTTTCAATTAAGAGGGT 3212
 QY 484 GGCTCAAGTCATGATATCAACCTGGGTGTCAATGACGAAACAGCCCGCATTTATATG 543
 DB 3211 GAAATGTTATTAATAAGATTAATCTATGTTGTCTTAACTATTCAGCAAGCAATTAATGG 3152
 QY 544 CATGTAACCATCTGACGCAATATATACAGAAATCAGACCGGAAATTAAGAGCAAAAG 603
 DB 3151 CATATATGATTTAATAAGCAATATATCAATATTTCTCTTATTCAGCAAGCAAAATTTA 3092

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OY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTGAAGAACTGTGCTGCGGCG 663
Db 3091 TTGGAAAGGTGTAAACATTAAGACCTTTAGGCAATGAAGCAATTTGGATTGCGAGGT 3032
OY 664 GATTATACAGCGCCCTCCCGGTTTGTCCAGAGCTGTTTATTGAAGAACTTAAGCGG 723
Db 3031 GGATTATCTTCACTGAGCGCTTGTGTGAATGCAATTTATGAAGCAAACTTGTCTCA 2972
OY 724 GCGGCGGATGAAGCAAGAGTGTAAACAGCCGCTTTCAAAATTTGGCAAAATGACGATA 783
Db 2971 AACATATGAAGAAATGATTTAATGAATGATTTTATTGAATGCGGTAATATTA 2912
OY 784 CCAAGGCGCGAGTGTAAACGGAAGAACGAATTCATTAATGCAATATACCTTCCGTG 843
Db 2911 CCGATTGAATTTGTCGTCGCGCATATGCTGCAATCACTATACGATGATCAGACCGTA 2852
OY 844 ATGTGCAACGAACCTGAAACTATCTATTCCACCATGATGACAAATCGGCAATCCAAA 903
Db 2851 ATAAATTTAACTACAAAGACGTTATATTAATTAATGAGTATGCGCAATGAATTAAGTACA 2792
OY 904 GTAAATTTATTTCAAGAACCTTGACTGTGTGAGCCTAAGTGTTCGCTAAAGCA 963
Db 2791 TTAAAGCTCAGATGATTTAATTAATGAAGAAAGATGAGATTTTAAAGCTTGAGAG 2732
OY 964 GAAGAGATTTATCATGAGCTTAATTA 989
Db 2731 CATATCACTATTAGAAAGTTGAATGA 2706

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RESULT 14
US-10-329-624-444/c
; Sequence 444, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;           Gil H. Choi
;           Patrick S. Dillon
;           Craig A. Rosen
;           Steven C. Barash
;           Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/329,624
;   FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/956,171
;   FILING DATE: October 20, 1997
;   APPLICATION NUMBER: 60/009,861
;   FILING DATE: January 5, 1996
;   APPLICATION NUMBER: 08/781,986
;   FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Mark J. Hyman
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 444:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1146 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 444:
US-10-329-624-444

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Query Match      14.7%; Score 146; DB 7; Length 11466;
Best Local Similarity 47.5%; Pred. No. 2.9e-32;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

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OY 4 ATGTGCAACGACTTAACTTGAAGAACTGCTGACCGTAAACATGTAATTAAGCAAGCAATG 63
Db 3688 ATGTGCAACGACTTAACTTGAAGAACTTAAATATCAAGTACTTGTGACGACGATG 3629
OY 64 GATTTCGATTTTCAGCTGCGGACGAGAGTGATTTCTATCCGCCCGTTACAGCTGGAAC 123
Db 3528 GATTATGATTTATCAATTAAGATGTTGCCACAGAGTACGCTTAAGAAATTAATCGTTGGAAA 3569
OY 124 AGTGAAGCTGACGGAAGGCGCCATCAGACACAGTACGCGTTATCGGTATGCGGAGAAA 183
Db 3568 TCTTGCACT--GGACAGACAGCGCCAAACGCAATATGCTTTATTTGGCAGCAAGACAT 3512
OY 184 CTTGAAATATATATTTATTTGCGGACGCGCATTAATGAAGCGGTTTATCTTGTGCGCGCTT 243
Db 3511 ATGGAAGTTTATTTATTTATGATGATGTTTATGAATGAATGCGGCTTGCAATTAACACAA 3452
OY 244 TATTTTCGCGGCTATGCGGAGTACGAAAGAAACGATAGCGGAAGTATCCGTTCACTATGTC 303
Db 3451 TATTTTCGAGGTATATGATTTCAATATGATCAACACAAAGCGGAGTAAATATTAACG 3392
OY 304 CCGCATGAGTTTGTGACATGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
Db 3391 CAATATGATTTTGTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3332
OY 364 AAGATTCGATCTTAAAGATTTGAGAGAAAGAAATTAATGATCTATGATACAGTTTACCG 423
Db 3331 CAAGCATCCCAATATACATGTTGTGATGCTGTATATTAATGACATCGGTAAGTTCCGCCA 3272
OY 424 CTTACATGATTTGTGACAGCCGAGCCGCGGAAACCTGACATGACATGACATGACATGAC 483
Db 3271 TTGATTAATCAATGTTCCGATGACATGACATGACATGACATGACATGACATGACATGAC 3212
OY 484 GCGCTCAAGCTATGATTAATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Db 3211 GAATGTTATTAAGAAATTAATCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3152
OY 544 CATGTAAACGATCTGACAGCAATATACAGATCAGACCGAAGCAATTAAGAGCAAGAG 603
Db 3151 CATATATGTAATTAAGACATATATATCAATATTTCTCTTATTCAGACAAACGAAATTTA 3092
OY 604 ATGGCGGATTAAGCCCTTCTGCTTTGGCCAAAGCTTGAAGAACTGTGCTGCGGCGG 663
Db 3091 TTGGAAAGGTGTAAACATTAAGACCTTTAGGCAATGAAGCAATTTGGATTGCGAGGT 3032
OY 664 GATTATACAGCGCCCTCCCGGTTTGTCCAGAGCTGTTTATTGAAGAACTTAAGCGG 723
Db 3031 GGATTATCTTCACTGAGCGCTTGTGTGAATGCAATTTATGAAGCAAACTTGTCTCA 2972
OY 724 GCGGCGGATGAAGCAAGAGTGTAAACAGCCGCTTTCAAAATTTGGCAAAATGACGATA 783
Db 2971 AACATATGAAGAAATGATTTAATGAATGATTTTATTGAATGCGGTAATATTA 2912
OY 784 CCAAGGCGCGAGTGTAAACGGAAGAACGAATTCATTAATGCAATATACCTTCCGTG 843
Db 2911 CCGATTGAATTTGTCGTCGCGCATATGCTGCAATCACTATACGATGATCAGACCGTA 2852
OY 844 ATGTGCAACGAACCTGAAACTATCTATTCCACCATGATGACAAATCGGCAATCCAAA 903
Db 2851 ATAAATTTAACTACAAAGACGTTATATTAATGAATGATTTTAAAGCTTGAGAG 2792
OY 904 GTAAATTTATTTCAAGAACCTTGAAGCTTTGAGAGCTTAAGTGTTCGCTAAAGCA 963

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Db	2791	TTTAAAGCTCAGATGATTTAATTATATGAAAAGATATGCGATTTTAAAGCTCAGAG	2732
Qy	964	GAAGAGTATTCATGAGCTTAATTA	989
Db	2731	CATATCACTATTAGAAAGTTGATATA	2706

RESULT 15

```

? Sequence 8383, Application US/09815242
? Patent No. US20020061559A1
? General Information:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlsen, Kari L.
? APPLICANT: Zyckind, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? TITLE OF INVENTION: Prokaryotes
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815,242
? CURRENT FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 8383
? LENGTH: 1002
? TYPE: DNA
? ORGANISM: Staphylococcus aureus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(1002)
? US-09-815-242-8383

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Query Match	14.3%	Score 142.8;	DB 3;	Length 1002;
Best Local Similarity	47.3%	Pred. No. 7.2e-32;		
Matches 466; Conservative	0;	Mismatches 517;	Indels 3;	Gaps 1

[illegible]

Dd	247	TATTTCCGAGGTTATAGTTCAATATAGGCTCACAACAAGGCGATGCCATGAATATTAAG	306
Qy	304	CCGCAATGAGTTTGTGACATGAGGCTGTCACTCTGTCACTCTTTGGAGAAGCTAAAGAA	363
Dd	307	CAAAATGAAATTTGTGACATGATGATTTTGGGATATATCAACAGCATTTGMAATATGAACA	366
Qy	364	AAGATTCGATCTTTAACCATTGTATAGAGAAAAATTAGATCTATTTGGATACAGTTTACCG	423
Dd	367	CAAGCATCCAAATACATAGTTGTAGCTGTATATTTAAATGATATGCGTAAAGTTCCGCCA	426
Qy	424	CTTGACCTGATATATGTGACAGCCGAGCGGACGAAACTGACGATAGAACCAAGACAGAC	483
Dd	427	TTGCATTATCAATGTTTCCGATGCAACTGCACTTCACTGCGAAGTTTCACTTTAAAGGGGT	486
Qy	484	GGCCTCAAAAGTCTATGATATATCAACTGTGTGTCATGACGAACAGCCCGACCTTATATGG	543
Dd	487	GAAAGATATTAATAAAGATATACCCATTTGTGTGTCTTAAACAAATCATCTCAAGCTTAAATGG	546
Qy	544	CATGTATCAACTCTGACAGCATATACAGAAATCAAGATCCGAGCAATTAGAGCAAAAG	603
Dd	547	CATTATATTAATTTAAGAACAATATATCAATATTTCTCTTATCCAGCAACGAAATTTA	606
Qy	604	ATGGCGGATTAGCCCTTGTGCTTTTGAGCCAAAGCTTAGAACTGTGTGTCGCCGGG	663
Dd	607	TTGGAAAGTGAAACATTTAGACCTTTAGCAATGAAGCAGTACATTTGGATTGCCAGGT	666
Qy	664	GATTATACACGCGCTTCCCGGTTTGTCAAGCTGTATTTTGAAGAACAATTAGAGCCG	723
Dd	667	GGATTTATCTTCACTGACGCGCTTGTGTGAAGATGGCATTTATGAAGCAAACTTGCCTCA	726
Qy	724	GCGGCGCATGAACGAAGGTGTAAACGCGCTTTTCAAATTTTGGCAATATAGACGAT	783
Dd	727	AACATGATTAAGAATAGATTTAATGATGATGATTTATTTATATATGATCGCGGTAAATATA	786
Qy	784	CCAAAGGCGCAGGTATAAACGGAABAAGCAAAATTCATTATACGCAATATATCTCGTG	843
Dd	787	CCGATTGAAATTTGACGTCGCCATAGTGTGCAATCATATATACATATGATGACACGTA	846
Qy	844	ATGTGCAACGAACCTGAAACTTACTATTTTCCACCATATGACATGCGGCAATCCAAAA	903
Dd	847	ATTAATTTAATCAAGAAAGCTTAATATATTAAGTATTAATGGGCAATGAAATATAGTGCA	906
Qy	904	GTAATTTATTTTCATGAAGACTTGACGTGTGGAGCCTTAAAGTGTTTCCGCTAAAGCA	963
Dd	907	TTAAAGCTACAGATGATTTAATTAATGAAAAAGATATGACGATTTTAAAGCTGGAAG	966
Qy	964	GAAAGAGATTTTCATGAGCTTAATTA	989
Dd	967	CATATCACTATTTAAAAAGTTGAATGA	992

Search completed: March 18, 2006, 13:28:30
Job time : 998 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:54:08 ; Search time 452 Seconds
(without alignments)
5138.006 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996
1 catatgtgcacaaagctctac.....atgagcttaataaagatcc 996

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New.*
1: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/1/pubpna/PCR_NEW_PUB.seq.*
5: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.1.*
7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.1.*
8: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.1.*
9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.2.*
10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.3.*
11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.4.*
12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.5.*
13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	16.0	990	US-10-793-626-413	Sequence 413, App
2	159	16.0	2975	US-10-793-626-3345	Sequence 3345, Ap
3	159	16.0	4114	US-10-793-626-4184	Sequence 4184, Ap
4	93	9.3	975	US-11-074-176-367	Sequence 367, App
5	83.8	8.4	975	US-11-074-176-369	Sequence 369, App
6	38.8	3.9	720	US-10-750-623-59863	Sequence 59863, A
7	38.8	3.9	720	US-10-750-623-59863	Sequence 59863, A
8	36.2	3.6	1272	US-11-096-668A-29311	Sequence 29311, A
9	35.8	3.6	583	US-09-925-065A-392869	Sequence 392869, A
10	35.4	3.6	419	US-09-925-065A-654182	Sequence 654182, A
11	35.4	3.6	419	US-09-925-065A-654183	Sequence 654183, A
12	35.4	3.6	5901	US-10-932-182A-2969	Sequence 2969, Ap
13	35.4	3.6	5901	US-10-932-182A-2969	Sequence 2969, Ap
14	35	3.5	961	US-11-072-175-102	Sequence 102, App
15	34.6	3.5	583	US-09-925-065A-392868	Sequence 392868, A
16	34.4	3.5	4429	US-10-753-195-9	Sequence 9, Appl1
17	34.2	3.4	583	US-09-925-065A-392870	Sequence 392870, A
18	34.2	3.4	1835	US-09-925-065A-45229	Sequence 45228, A
19	34.2	3.4	1835	US-09-925-065A-45229	Sequence 45228, A
20	34.2	3.4	1835	US-09-925-065A-45230	Sequence 45230, A

21	34	3.4	601	US-09-925-065A-348226	Sequence 348226, A
22	34	3.4	193084	US-11-121-086-82	Sequence 82, Appl1
23	33.8	3.4	670	US-09-925-065A-556802	Sequence 556802, A
24	33.6	3.4	523	US-09-925-065A-155341	Sequence 155341, A
25	33.6	3.4	556	US-09-925-065A-777072	Sequence 777072, A
26	33.4	3.4	570	US-09-925-065A-29670	Sequence 29670, A
27	33.4	3.4	512	US-09-925-065A-321496	Sequence 321496, A
28	33.4	3.4	653	US-09-925-065A-96912	Sequence 96912, A
29	33.4	3.4	659	US-09-925-065A-510272	Sequence 510272, A
30	33.4	3.4	958	US-09-925-065A-713894	Sequence 713894, A
31	33.4	3.4	958	US-09-925-065A-713895	Sequence 713895, A
32	33.4	3.4	1187	US-10-750-185-62875	Sequence 62875, A
33	33.4	3.4	1187	US-10-750-185-62875	Sequence 62875, A
34	33.4	3.4	1217	US-09-925-065A-668875	Sequence 668875, A
35	33.4	3.4	2830	US-09-925-065A-669245	Sequence 669245, A
36	33.4	3.4	2830	US-09-925-065A-669246	Sequence 669246, A
37	33.2	3.3	629	US-09-925-065A-346097	Sequence 346097, A
38	33.2	3.3	645	US-09-925-065A-860511	Sequence 860511, A
39	33.2	3.3	961	US-09-925-065A-690516	Sequence 690516, A
40	33.2	3.3	2037	US-10-932-182A-1230	Sequence 1230, Ap
41	33.2	3.3	2037	US-10-932-182A-1230	Sequence 1230, Ap
42	33.2	3.3	156297	US-11-121-086-65	Sequence 65, Appl1
43	33	3.3	393	US-09-925-065A-184812	Sequence 184812, A
44	33	3.3	499	US-09-925-065A-845854	Sequence 845854, A
45	33	3.3	566	US-09-925-065A-828854	Sequence 828854, A

ALIGNMENTS

RESULT 1
US-10-793-626-413
Sequence 413, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
FILE REFERENCE: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: PUA3480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164, 258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 413
LENGTH: 990
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-413

Query Match 16.0%, Score 159, DB 8, Length 990;
Best Local Similarity 49.8%, Pred. No. 2e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY	2	ATATGTCACAAAGCTTACATGGAAGCTGACCGCTTAACATGATAGCAAGAACAA	61
DB	8	ATATGTCACAAAGCTTACATGGAAGCTGACCGCTTAACATGATAGCAAGAACAA	67
QY	62	TGATTTTCATTTTCAGCTGCGGACAGAGTATCTCTATCCGCGCTTACAGCTGGA	121
DB	68	TGATTTTCATTTTCAGCTGCGGACAGAGTATCTCTATCCGCGCTTACAGCTGGA	127
QY	122	ACAGTGAAGCTGACGAGAGCGCCATCAGACACAGTACCGCTTATCGGTAGGGAGAA	181
DB	128	AATTTGATCTTACATTCAGACATGCGCTTCTTGAATGTTTGTGAAACAATTTAA	184
QY	182	AACCTGGAATATATATTTATGCGGACCGCATTAAGAAAGCGTTATCTGTGCGGCGC	241
DB	185	AAATGAGAGCTTATAGATTTGTGATGATTAACCAAAAAGGTTTACATTTGCAACC	244

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Oy 242 TTTATTTCCGGGCTATGCGAGTACGAAAAACGATACGGGAGATACCGTTCATTTG 301
Db 245 ATTACTTCATCGTGGAGAGCTTCATACAGTACCCATTAACGTTATTTTAACTTAG 304
Oy 302 TCCCGCATGAGTTTGTGACATGGGTCTGTGATCTGTCACTTTTGAAGACGTAAG 361
Db 305 CACCTGAGAGTTTATTTTGGGTTTATAGTTTATTAAGATTTAGCCAAATTAAC 364
Oy 362 AAAAGATTCGATCTTTACGATTTGAGAGAAAAATTAGATCTATGATACAGTTTAC 421
Db 365 AAAAGGTTAAGAAAATCATATTTATGAAATGAAAAAATACGACTTGAATTCGTTCTC 424
Oy 422 CGCTTCACTGATATTTGTCAAGCGGAGCGGAAACCTGACATAGAACCAAGAGAG 481
Db 425 CTTTACATTTTCAATGCTCCTGATGAAACAGACATACCTGACCTTACATG 484
Oy 482 ACGGCTTCAGAGTCTATGATATCAACCTGTGTGATGACGAAACGCCGACTTATAT 541
Db 485 GCTTATTTAATGTTAAAGATATATTTGTTCAATCCTTAACAAATGAACTTAATGAT 544
Oy 542 GGCATTTACCAATTTGACGATATACAGAAATCAGACCAAGCAATTTAGAGCAAG 601
Db 545 GGCATCTATCTTAACTTAAAGAAATTAAGCTTTTAAACGCCACAGAAATCAACATCAT 604
Oy 602 AGATGGGGGAGTTAGCCCTTTCTGCTTTGGCCAGGCTTACGAACTGTGGCTGCCG 661
Db 605 TAAATAGTAAAGTGTAGTAAATGATCAATGGCTGTGAAGCAGAAACAAATGGCTTACC 664
Oy 662 GGGATTATACACCGCTTCCCGTTTGTCAAGCTGTTATTTGAAGAACATCTAGAGC 721
Db 665 GTGGTTATACGTCAACAGATGTTTTATACGGCTACATATTTAGACCAACCACTACCT 724
Oy 722 CGGGGCGGAGTAAACGAAAGTGTAAACGCCCTTTCAATTTTGGCAATATAGAGA 781
Db 725 GTTCCATATGAAATGAAATTTAATGAAATTTTAAAGTTCTAGATCAGTACGA 784
Oy 782 TACCAAGGGGCGAGTAAACGAAAGAAAGCAAAATTCATATACGAAATTAATCTTCG 841
Db 785 TCCCTCAAGGTGCACTTAT---CGATGCCAATTAATTAATACACATATCAATTAG 841
Oy 842 TGATGTGCAACGAACTGAAACCTATTTCCACCACTAGACATAGCGCAATTCGAA 901
Db 842 TGATGGAAGTAAAGAAAGATTTATATTAAGCTTACCTTAGCAATCAAAATTTCA 901
Oy 902 AAGTAAATTTATTTTCATGA 920
Db 902 AAATAAATTAACGAAAG 920

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RESULT 2

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US-10-793-626-3345/c
; Sequence 3345, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU480US
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3345
; LENGTH: 2975
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3345

```

Query Match

16.0%; Score 159; DB 8; Length 2975;

Best Local Similarity 49.8%; Pred. No. 3,4e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

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Oy 2 ATATGTCACAAGCTTACATTTGGAACCTGTCAGCGTAAACATGATTAAGCAAGAA 61
Db 1755 ATATGTCAGTCCATTTCTTTATATACAAACAGCTACCATTTATTTACTTGAACA 1686
Oy 62 TGAATTTGCAATTTCACTGGGAGCAGAGGTGATTTCTATCCGCGCGTTACAGCTGGA 121
Db 1695 TGAATTTGCAATTTGATTTAATGATATCCCAACCATTTGTTCCAGCCATATCATACC 1636
Oy 122 ACAGTGAAGCTGACGGAAGGCCCATACAGACAGTACGCTTTATGCTATGGGAGAA 181
Db 1635 AATTGATCTAGATTCAGACATGGCTCTT---GATATGTTTGTGTGAAACAAATTTAA 1579
Oy 182 AACTGGAATATATTTATTTTCCGAGCGCATTAATGAAGGGTTATCTTGCGGGCGC 241
Db 1578 AAGTAGACCTTATAGATTTGTTGATGATTAAGAAAGGTTTACCTTTTCGAAC 1519
Oy 242 TTTATTTCCGGGCTATGCGAGTACGAAAAACGATACGGGAGATACCGTTCAATTTG 301
Db 1518 ATTACTTCATCGTGGAGAGCTTCATACAGTACCATTAACGTTATGTTATTTAACTTAG 1459
Oy 302 TCCCGCATGAGTTTGTGACATGGGTCTGTGATCTGTCACTCTTTGGAAGACGTAAG 361
Db 1458 CACCTGAGAGTTTATTTGTTGGGTTTAAAGTTTAAATTAAGATTAAGCAATTTAAAC 1399
Oy 362 AAAAGATTCGATCTTTAAGATTTGTAGAGAAAAAATTAAGATCTATGATACATTTTAC 421
Db 1398 AAAAGGTTAAGAAATCATATTTATGAAATGAAAAAATACGACTTTGAATTCGTTCTC 1339
Oy 422 CGCTTCACTGATATTTGTCAAGCCGAGCGGCGGAAACCTGACATTAAGAACCAAGAGAG 481
Db 1338 CTTTACATTTTATGATGATCACTGATGAAACAGACATACGATGATGAACTTCAATG 1279
Oy 482 ACGGCTTCAGAGTCTATGATATCAACCTGTGTGATGACGAAACAGCCCGCATTTAT 541
Db 1278 GCTTATTAATGTTAAGATATATATGTTCAATCTTAAACAAATGAACCTTAATTAAT 1219
Oy 542 GGCATGTAACCAATCTGAGCAATATACAGAAATCAGACCGAACAATTAAGAGCAAG 601
Db 1218 GGCATCTATCTTAACTTAAAGAAATTAAGCTTTTAAAGCCACAGAAATCAACATCAAT 1159
Oy 602 AGATGGGCGAGTTAGCCCTTTCTGCTTTTGGCCAAAGCTTAAAGAACTGTGTGCGG 661
Db 1158 TAAATAGTAAAGTGTAGTAAATGATCAATGGCTGTGAAGCAGAAACAATGGCTTACC 1099
Oy 662 GGGATTATACACCGCTTCCCGTTTGTCAAGCTGTTATTTGAAGAAACATCTAGAGC 721
Db 1098 GTGGTTATACGTCAACAGATGTTTTTAAACCGGCTACATATTTAAGACCAACATACCT 1039
Oy 722 CGGGGCGGAGTAAACGAAAGTGTAAACAGCGCTTTCAATTTTGGCAATATAGAGA 781
Db 1038 GTTCCATATGAAAGATGAAATTTAATGAAATTTTAAAGTTCTTAAATCAGTACGTA 979
Oy 782 TACCAAGGGGCGAGTAAACGAAAGAAAGCAAAATTCATTAACGCAATTAATCTTCG 841
Db 978 TCCCTCAAGGTGCACTTAT---CGATGCCAATTAATTAATACACATATCAATTAG 922
Oy 842 TGATGTGCAACGAACTGAAACCTATTTCCACCACTAGACATAGCGCAATTCGAA 901
Db 921 TGATGGAAGTAAAGAAAGATTTATATTAAGCTTACCTTAGCAATCAAAATTTCA 862
Oy 902 AAGTAAATTTATTTTCATGA 920
Db 861 AAATAAATTAACGAAAG 843

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RESULT 3

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US-10-793-626-4184
; Sequence 4184, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

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APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIORITY FILING DATE: 1999-11-09
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4184
LENGTH: 4114
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4184

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Query Match      16.0%; Score 159; DB 8; Length 4114;
Best Local Similarity 49.8%; Pred. No. 4e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

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QY 2 ATATGTCACAGTCTTACATGGAACTGCTGACCGTAAACATGATTTAGCAAGACAA 61
DB 1626 ATATGTCACAGTCTTACATGGAACTGCTGACCGTAAACATGATTTAGCAAGACAA 1685
QY 62 TGGATTTTGGATTTGACCTGCGGACAGAGGTGATTTCTTATCCGCGCGCTTACAGCTGA 121
DB 1686 TGGATTTTGGATTTGACCTGCGGACAGAGGTGATTTCTTATCCGCGCGCTTACAGCTGA 1745
QY 122 ACAGTGAAGTGCACGAGAGGCGCCATGACACAGTACCGCTTATCGGTATGGGAGAA 181
DB 1746 AATTTGATCTGATGATTCAGACATGCTCTT---GAAATGCTTTTGTGGAAACAAATTTAA 1802
QY 182 AACTGGAATATATATTTATTTGCGAGCGCATTAATGAAACGGTTATCTTGGCGCGC 241
DB 1803 AACTGGAATATATATTTATTTGCGAGCGCATTAATGAAACGGTTATCTTGGCGCGC 1862
QY 242 TTTATTTTCCGGCTATGCGAGTACGAAAAAGATACCGGAGATACCGTTCAGATTG 301
DB 1863 ATTACTTCACTGCTGAGAGGCTCATACAGTACCCATTAAGCTTATGTTATTTAATCTAG 1922
QY 302 TCCCGCATGATTTGACAGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
DB 1923 CACTGAGAGTATTTGTTGGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAAAC 1982
QY 362 AAAAGATGATTTTAAAGATTTGATGAGAAATTTAGATCTATTTGATGATGATTTTAC 421
DB 1983 AAAAGATGATTTTAAAGATTTGATGAGAAATTTAGATCTATTTGATGATGATTTTAC 2042
QY 422 CGCTTCACTGATATTTGTCAGACCGGACCGGCGGAAACCTGACGATGAAACCAAGACAG 481
DB 2043 CTTTATATTTCACTGATATTTGTCAGACCGGACCGGCGGAAACCTGACGATGAAACCAAG 2102
QY 482 ACGGCTCAAAGTCTATGATATCAACCTGCTCATGACGAAACAGCCCGACTTATAT 541
DB 2103 GCTTATATTAATGATTAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 2162
QY 542 GGCATGTAACCATCTGACGATATATACAGATATACAGGATACCGAAGCATTTAGAGAGAAAG 601
DB 2163 GGCATGTAACCATCTGACGATATATACAGATATATACAGGATATACCGAAGCATTTAGAG 2222
QY 602 AGATGGCGGATTAAGCCCTTTCTGCTTTGGCGAAGCTTAGGACGTTGCTGCTGCTGCTGCTG 661
DB 2223 TATATGTAAGATGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2282
QY 662 GGGATTAATACACCGCTTCCGCTTTGCTGACAGCTGTTATTTTGAAGAAACATCTAGAC 721
DB 2283 GTGCTTATATGCTACAGATGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2342
QY 722 CGGCGCGGATGAAAGAAAGGTGTAACGCGCTTTGAAATTTTGGGAAATATGACGA 781
DB 2343 GTTCCATATATGAAAGTAAATTTTATGATGATGTTTAAAGTTCTAGAAATGACGATGAT 2402

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QY 782 TACCAAGGCGGATGATTAACGGAAGAAAGCAAAATTCATTAACGCAATATATCTCG 841
DB 2403 TCCTCAAGGTGATGATTT---CGATGCCAATTAATATATATATATATATATATATATAT 2459
QY 842 TGATGTCACAGAACTGGAATCTATTTTCCACATATGACATATGCAATGCGCAATCCAA 901
DB 2460 TGATGTCACAGAACTGGAATCTATTTTCCACATATGACATATGCAATGCAATATTTCA 2519
QY 902 AAGTAAATTTATTTATGTA 920
DB 2520 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2538

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RESULT 4
US-11-074-176-367
Sequence 367, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAniff, Olivia
APPLICANT: Pettit, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIORITY FILING DATE: 2004-03-08
PRIORITY FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 367
LENGTH: 975
TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(975)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: ORF 892; bsha
US-11-074-176-367

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Query Match      9.3%; Score 93; DB 12; Length 975;
Best Local Similarity 46.4%; Pred. No. 2e-16;
Matches 340; Conservative 0; Mismatches 390; Indels 3; Gaps 1;
QY 197 TATTTGCGAGCGCATTAATGAAAGCGGTTTCTTGTGCGGCGCTTATTTTCCGGGCT 256
DB 188 TATATTTGCGAGCGCATTAATGAAAGCGGTTTCTTGTGCGGCGCTTATTTTCCGGGCT 247
QY 257 ATGCGAGTACGAAAAAGATACGGAAGATACCGTTCATATGCTCCGATGAGTTTG 316
DB 248 ATGCTACATATATATGAAAGAAAA---GAAATTAAGATATATGCTTCTTGAATTTCA 304
QY 317 TGAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
DB 305 TCCCTTGAATTTTGAAGACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 364
QY 377 TAAAGTGTGTAAGAAAAATATGATCTATGATGATGATGATGATGATGATGATGATGATGAT 436
DB 365 TCAATGCGCGCATTTAAATTTTCAAGGAAAAATGCAAGCTTCTTCTTCACTGCTTCA 424
QY 437 TGTCAAGCGGACGGCGCGGAACTGACGATGAAACCAAGACAGACGCGCTCAAGTCT 496
DB 425 TTGCAAGATTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 497 ATGATATATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
DB 485 ATGATATATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544

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Oy 557 TGACGACATATATACAGGATACAGCCGACATATAGAGCAAGATGGCGGATTAG 616
Db 545 TAAATTAATTAATGCTGACGATATCTCCAAAATGCTTAAATAATCTTCAAGATAAGTAA 604
Oy 617 CCCTTCTGCTTTTGGCCAAAGGCTTAGAACTGTGTCTGCGCGGGGATATATACACCGC 676
Db 605 AATAGGCTGGCTACAGCCGCTGATAGGCTGTCAACAATTAACAGGTGAATGATTCG 664
Oy 677 CTTCGGGCTTTGTCAGAGCTGTTTATTTGAAAGAACATCTAGAGCGCGCCCATGAAA 736
Db 665 AATACGTTTGTGAGATAGCTTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 724
Oy 737 CGAAAGGTGTAACAGCGCTTTTCAATTTTGGCAATATATGACATACAAAGGCGGAG 796
Db 725 AAGAAATATATGATATCTTACTTCCATTTTACATTCGCTTGAACAAAGGAGACTGG 784
Oy 797 TGATTAACGGAAGAGACCAATTCATTTATACGCAATATATCTTCCGTGATGTCACAA 856
Db 785 ATGAAGTTGTGTCAAACATCATTTGATATATACAAATTTATTCGATGGAATGATGACA 844
Oy 857 CTGGAATCTACTATTTCACACCATCTATGACATCGCAATCCAAAAGTAAATTTATTC 916
Db 845 AAGGATTTTCTACTACACCACTTATTCAAACAAACAAATTAACGTTGTATGATGA 904
Oy 917 ATGAAGACTTGA 929
Db 905 AAGAGATCTAGA 917

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RESULT 5

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US-11-074-176-369
; Sequence 369, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(975)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1078; bshb
US-11-074-176-369

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Query Match 8.4%; Score 83.8; DB 12; Length 975;

Best Local Similarity 45.4%; Pred. No. 8.9e-14;

Matches 341; Conservative 0; Mismatches 407; Indels 3; Gaps 1;

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Oy 181 AAACCTGGAATATATATTTCCGACGCGCATTAATGAAGCGTTATCTTGTGCGGCG 240
Db 172 AATGATGATATCATCTATATATGATGATGCAATTAATGAAGGCGCTGTGATGACAGA 231
Oy 241 CTTTATTTTCCGGGCTATGCGAGTACGAAAAAGCATACGGAGAGATCCGTTACATT 300
Db 232 TTAATATTTCAAGG--TCTTAATCATTACTTTCTTAATATGAAGTAAAGATATAT 288

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Oy 301 GTCCCGCATGATTTTGACATGGGTGCTGTCACTGTCACTCTTGTGAAGAGTAAA 360
Db 289 GCTTCTTTGATTTAATGACATCTTATTAAGTAATTTGTGAATAATGATGACGATGTTAAA 348
Oy 361 GAAAGATTGATCTTTAATGATTTGAGAGAAAAAATTAAATCTATTTGATACGTTTA 420
Db 349 GAAATCTTAATATGCAAAATATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 408
Oy 421 CCGCTTACATGATATGTGACAGCCGAGCGGAGAAACCTGACATAGAACCAAGACA 480
Db 409 GATTATCATTTGATTTAATGATTAAGTATTAAGCTGTGATAGATATTCGATGATCAACAT 468
Oy 481 GACGCGCTCAAGATCTATGATTAATCAACCTGTGTCTATGACGACAGCCCGACTTATA 540
Db 469 TGAGTTTACATATTTATGATTAATCCAGTAATGTCTTAATCAATCCGAAATTCG 528
Oy 541 TGGCATTTAACCAATCTGACAGCAATATACAGAAATCAGCCGAAACATTAAGAGCANA 600
Db 529 GATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 588
Oy 601 GAGATGGCGGATTAAGCCCTTCTGCTTTTGGCCAGGCTTAGGAGCTGTGCTGCG 660
Db 589 TTGTTCTTAATGTTGATCTTAATCTATATATATATATATATATATATATATATATAT 648
Oy 661 GGGGATTAATACACCGCTTCCGCTTGTGACAGCTGTTATTTGAAAGACATCTAGAG 720
Db 649 GGTGGAATGATTTACTCTCTCATTTGTTAAGTACTTTTGTCTGGCACAATCTCA 708
Oy 721 CCGGCGGCGCATGAACGAAAGGTGTAACAGCCGCTTTCAATTTTGGCAATATGACG 780
Db 709 CAAGGAAAAATGAAAGGAAATATGTAATTAATTAATTAATTAATTAATTAATTAATTA 768
Oy 781 ATACCAAGGCGGAGATTAAGGAAAGAGACAAATTCATTAAGCAATATCTTCC 840
Db 769 CAACCTGATGTTTATGATGAAATGAAAGTAAAGATATATGCTATGATATATATATAT 828
Oy 841 GTGATGTGACAGAACTGAACTGAACTATTTCCACCATATGACATCGGCAAAATCCAA 900
Db 829 TGTATGAATTAATGATTAAGGATTTTGTACTTACTTATGACAAATTAATCGATTAT 888
Oy 901 AAGTAAATTTATTTCAATGAAGCTTGACT 931
Db 889 GCAGTATATGATTAAGCAATTAAGATTTAGATT 919

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RESULT 6

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US-10-750-185-59863/c
; Sequence 59863, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59863
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-59863

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Query Match 3.9%; Score 38.8; DB 8; Length 720;

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108827.135
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 654182
;; LENGTH: 419
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-654182

Query Match 3.6%; Score 35.4; DB 6; Length 419;
Best Local Similarity 57.8%; Pred. No. 5.1;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 333 AGTGTGACGCTTGAAGCGTAAAGAAAGATTGATCTTAAAGATTGAGAGAA 392
Db 244 AGATTAAACGAATTTAAGAAACAGATTTTAAAGATTAATTAACCACTTTATGAGA 303
Qy 393 AAAATTGATCTATTGATACAGTTTACCGCTTCACTGATTTGTGA 441
Db 304 TAAATTGATGACAGATTTATTTTCTTCGAATCTGTAATTTGTTA 352

RESULT 11
US-09-925-065A-654183
;; Sequence 654183, Application US/09925065A
;; Publication No. US20040181048A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108827.135
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 654183
;; LENGTH: 419
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-654183

Query Match 3.6%; Score 35.4; DB 6; Length 419;
Best Local Similarity 57.8%; Pred. No. 5.1;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 333 AGTGTGACGCTTGAAGCGTAAAGAAAGATTGATCTTAAAGATTGAGAGAA 392
Db 244 AGATTAAACGAATTTAAGAAACAGATTTTAAAGATTAATTAACCACTTTATGAGA 303

Qy 393 AAAATTGATCTATTGATACAGTTTACCGCTTCACTGATTTGTGA 441
Db 304 TAAATTGATGACAGATTTATTTTCTTCGAATCTGTAATTTGTTA 352
RESULT 12
US-10-932-182A-2969
;; Sequence 2969, Application US/10932182A
;; Publication No. US20060046253A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAO, YOSHIHIRO
;; APPLICANT: KODAMA, YUKIKO
;; APPLICANT: FUJIMURA, TOMOKO
;; APPLICANT: ASHIKARI, TOSHIHIKO
;; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;; FILE REFERENCE: 030685-043
;; CURRENT APPLICATION NUMBER: US/10/932,182A
;; CURRENT FILING DATE: 2004-09-02
;; NUMBER OF SEQ ID NOS: 197023
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 2969
;; LENGTH: 5901
;; TYPE: DNA
;; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2969

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
Best Local Similarity 50.9%; Pred. No. 19;
Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 693 AGCTGTTATTGAAAGACATCTAGAGCGCGCGCGATGAACGAAGGTGTAACAC 752
Db 894 AGCTTATACACGATGAATATATGTTGATTTGCCCTACAGTGCAGGTGAACAGA 953
Qy 753 CGCTTTCAATTTTGGCAATATGACATACCAAGGCGCAGTGAACGAAGAGA 812
Db 954 CGTTCACCTACTTACGATTTTAAACACGTTAAACAGTTTCTCGTATCAACGAGAAA 1013
Qy 813 CGAATTCAATTATACGCAATATCTTCCGTGATGTGCAAGAAC 857
Db 1014 CGAATTGATATACATACGATAGTTTCAAGGTTGTCTAGCTAGC 1058

RESULT 13
US-10-932-182A-2969
;; Sequence 2969, Application US/10932182A
;; Publication No. US20060046253A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAO, YOSHIHIRO
;; APPLICANT: NAKAMURA, NORIHISA
;; APPLICANT: KODAMA, YUKIKO
;; APPLICANT: FUJIMURA, TOMOKO
;; APPLICANT: ASHIKARI, TOSHIHIKO
;; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;; FILE REFERENCE: 030685-043
;; CURRENT APPLICATION NUMBER: US/10/932,182A
;; CURRENT FILING DATE: 2004-09-02
;; NUMBER OF SEQ ID NOS: 197023
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 2969
;; LENGTH: 5901
;; TYPE: DNA
;; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2969

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
Best Local Similarity 50.9%; Pred. No. 19;
Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 693 AGCTGTTATTGAAAGACATCTAGAGCGCGCGCGATGAACGAAGGTGTAACAC 752
Db 894 AGCTTATACACGATGAATATATGTTGATTTGCCCTACAGTGCAGGTGAACAGA 953

QY 753 CGCTTTCAATTGGCAATATGACGATACCAAGGCGCAGTGATAACGAGAGAGA 812
DB 954 CGTTGACACTACTACGATATTTAAACGCTAAACAGTTCTCCGTGATCAACGAGAAA 1013
QY 813 CGAATTCATTATACGCAATATCTCCGATGTGCAAGAAC 857
DB 1014 CGAATTCATTATACGCAATATCTCCGATGTGCAAGAAC 1058

RESULT 14

US-11-072-175-102
; Sequence 102, Application US/11072175
; Publication No. US20060299441
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; PRIOR FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 102
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-102

Query Match 3.5%; Score 35; DB 9; Length 961;
Best Local Similarity 47.1%; Pred. No. 10; Mismatches 120; Indels 0; Gaps 0;
Matches 107; Conservative 0;

QY 293 TTCACATGTCGCCGATGAGTTGTGACATGGGTGTCAGTCTGCACTTTTGAAG 352
DB 466 TTAACACAGTCATGAAAGTTGGCTTCGTTGATGTCTGTGGCGTGGCAAC 525
QY 353 AGCTAAAGAAAAGATTCATCTTTAAGCATTTAGAGAAAAATTGATCTATTGATA 412
DB 526 AGGAGACCACTATGAGATGTTCTGTGTTCAGTGAATAATCTATTCTATGAGA 585
QY 413 CAGTTTACCGCTGCTGATATGTCAGACCGGAGCGGCGCAACCTGAGATGAAC 472
DB 586 CATTTTCTTTATCCACAGTATTTTTCACACTGTATCATGAACTACCTTTAGAA 645
QY 473 CAGAGCAGACGGCTCAAGTCTATGATATCACTGCTGTCATG 519
DB 646 AATAAGATTACCTGCGCAAAAATAAGAGAAACGGAATGACGTTATG 692

RESULT 15
US-09-925-065A-392868/c
; Sequence 392868, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392868
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-392868

Query Match 3.5%; Score 34.6; DB 6; Length 583;
Best Local Similarity 49.7%; Pred. No. 10; Mismatches 89; Indels 0; Gaps 0;
Matches 88; Conservative 0;

QY 802 ACGAAGAGAGCAATTCATTATACGCAATATCTCCGTGATGCAACGAACTGGA 861
DB 341 ATGGAAGAGCTTAATGTATATTCACAGTAAAGACATCTGAAAGCTGCAT 282
QY 862 AACTACTATTTCCACCACTATGACATCGCAATCCAAAAGTAATTTATTCATGAA 921
DB 281 CTGATATGATTCACACTATATGACATTCAGAAAACAAAACATGTAATGTAAAA 222
QY 922 GACCTTGATGTTTGAAGCTTAAAGTTTTCGCTTAAAGCAGAGAGTATTCAT 978
DB 221 GATCAGTGTGTCACAGGGGAAAACGGGGGTGAACAGGTGCGCACAGAGATTCCT 165

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